

OM protein - protein search, using sw model
Run on: February 7, 2006, 16:36:57 ; Search time 199 Seconds
(without alignments)
759.529 Million cell updates/sec

Title: US-09-981-915A-523
Perfect score: 1806
Sequence: 1 MKTIQPMHNSISWAFTGL.....RRAGCVLLPLLVLLHLLKF 344
Scoring table: BLOSUM62
Searched: Gapop 10.0, Gapext 0.5
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
-----	-------	-------	--------	----	----	-------------

RESULT 1
ID AAY57601 standard; protein; 344 AA.

DE Human protein SEQ ID NO:1.

PN WO9958668-A1.

PD 18-NOV-1999.

PA (ONVOY) ONO PHARM CO LTD.

Query Match 100.0%; Score 1806; DB 3; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 2

ID AAB44329 standard; protein; 344 AA.

DE Human PRO337 protein sequence SEQ ID NO:523.

PN WO200053756-A2.

PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 3; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 3

ID AAB31204 standard; protein; 344 AA.

DE Amino acid sequence of human polypeptide PRO3337.

PN WO200077037-A2.

PD 21-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 4; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 4

ID AAU12359 standard; protein; 344 AA.

DE Human PRO337 polypeptide sequence.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 4; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 5

ID AAU83654 standard; protein; 344 AA.

DE Human PRO protein, Seq ID No 126.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 5; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 6

ID ABB84844 standard; protein; 344 AA.

DE Human PRO337 protein sequence SEQ ID NO:56.

PN WO200200690-A2.
PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 5; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 7

ID ABB95450 standard; protein; 344 AA.

DE Human angiogenesis related protein PRO337 SEQ ID NO: 56.

PN WO200208284-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERRITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GURN) GURNEY A L.

PA (HILL) HILLAN K J.

PA (MARS) MARSTERS S A.

PA (PANJ) PAN J.

PA (PAON) PAONI N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

Query Match 100.0%; Score 1806; DB 5; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 8

ID ADY31866 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO3337.

PN WO200193983-A1.

PD 13-DEC-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 5; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 9

ID ABO17803 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO3337.

PN US2003032156-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 10

ID ABU80801 standard; protein; 344 AA.

DE Human PRO polypeptide #63.

PN US2003036635-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 11

ID ABO25175 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO3337.

PN US2003040014-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 12

ID ABO25275 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO3337.

PN US2003050239-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 13

ID ABO33767 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO3337.

PN US2003045687-A1.

PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 14
ID ABU81057 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 15
ID ABU72281 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 16
ID ABU66757 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 17
ID ABU67293 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 18
ID ABU84961 standard; protein; 344 AA.
DE Human secreted and transmembrane PRO polypeptide #37.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 19
ID ABU59838 standard; protein; 344 AA.
DE Novel secreted and transmembrane protein PRO337.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 20
ID ABU61159 standard; protein; 344 AA.
DE Human PRO337 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 21
ID ABO25028 standard; protein; 344 AA.
DE Human secreted/transmembrane protein (PRO) #188.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 22
ID ABU72061 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 23
ID ABU67162 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
FN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 24
ID ABU80428 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
FN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 25
ID ABU82110 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
FN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 26
ID ABU67033 standard; protein; 344 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 376.
FN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 27
ID ABU79804 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
FN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 28
ID ADA45895 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
FN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 29
ID ADA76326 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
FN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 30
ID ABU72290 standard; protein; 344 AA.
DE Human PRO337 protein.
FN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 31
ID ADA18976 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
FN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 32
ID ADA18976 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
FN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 32
ID ADA61599 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 33
ID ADB19384 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 34
ID ADB27925 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 35
ID ADA86404 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 36
ID ADB15968 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 37
ID ADA47754 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 38
ID ADA67549 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 39
ID ADB30556 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 40
ID ADA85852 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;

RESULT 41
ID ADA97064 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 42
ID ADA79368 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 43
ID ADA87507 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 44
ID ADB16709 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 45
ID ADA91801 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 46
ID ADB14864 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 47
ID ADA25062 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 48
ID ADA47276 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 49
ID ADB18825 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 50
ID ADB18825 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;

ID ADA94040 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 51
ID ADB19936 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 52
ID ADB13248 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 53
ID ABO43336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 54
ID ABO19730 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 55
ID ADA12723 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US200305216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 56
ID ADA74502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 57
ID ADB24735 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 58
ID ADA82259 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 59
ID ADA75222 standard; protein; 344 AA.

DE Human PRO polypeptide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 60
ID ADA85300 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 61
ID ADA84748 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 62
ID ADB30004 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 63
ID ADA80532 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 64
ID ADA5774 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 65
ID ADA46999 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 66
ID ADB25295 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 67
ID ADA93471 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 68
ID ADB26821 standard; protein; 344 AA.
DE Human PRO polypeptide #188.

PN US20030922147-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 69
ID ADB31108 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 70
ID ABJ72418 standard; protein; 344 AA.
DE Human PRO337 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 71
ID ADA61036 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 72
ID ADB24183 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 73
ID ADA96512 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 74
ID ADA81084 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 75
ID ADA95960 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 76
ID ADB26269 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 77
ID ADB21754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082765-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 78
ID ABO34313 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO 337.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 79
ID ABO19621 standard; protein; 344 AA.
DE Novel human secreted and transmembrane polypeptide #89.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 80
ID ADA77533 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 81
ID ADB18273 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 82
ID ADA86956 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 83
ID ADA88059 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 84
ID ADA46447 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 85
ID ADB28477 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 86
ID ADB29029 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

```
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 87
ID ADA76981 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 88
ID ADA88611 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 89
ID ADA97616 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 90
ID ADB27373 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 91
ID ADB22306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 92
ID ABO19862 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 93
ID ABJ72120 standard; protein; 344 AA.
DE Human membrane bound receptor/protein PRO337 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 94
ID ADA66997 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 95
ID ADB22858 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 96
ID ADB66588 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 97
ID ADA92353 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 98
ID ADB15416 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 99
ID ADB83616 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 100
ID ADB80722 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 101
ID ADB73263 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 102
ID ADB38668 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 103
ID ADB78345 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 104
ID ADB38116 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 105
ID ADB66588 standard; protein; 344 AA.
```

DE Novel human secreted and transmembrane protein PRO337.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 106
ID ADB84993 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 107
ID ADB89668 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 108
ID ADB90400 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 109
ID ADB39501 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 110
ID ADB78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 111
ID ADB74029 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 112
ID ADB87165 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 113
ID ADB84747 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 114
ID ADB47124 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.

PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 115
ID ADB83862 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 116
ID ADB86731 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 117
ID ADB73017 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 118
ID ADB76745 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 119
ID ADB77336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 120
ID ADB34493 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 121
ID ADB35597 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 122
ID ADB33941 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 123
ID ADB35045 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077718-A1.

```
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 124
ID ADB36149 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 125
ID ADB46544 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 126
ID ADC44171 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 127
ID ADC61931 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 128
ID ADC63895 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 129
ID ADC66995 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 130
ID ADC69119 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 131
ID ADC63179 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003086648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 132
ID ADC68244 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 133
ID ADC41564 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 134
ID ADC67619 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 135
ID ADC62555 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 136
ID ADC36855 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 137
ID ADC42188 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 138
ID ADC21845 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 139
ID ADC50417 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 140
ID ADC71964 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 141
ID ADC59943 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
```

Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 142
ID ADC49876 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 143
ID ADC49075 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 144
ID ADC49592 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 145
ID ADC47453 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 146
ID ADC52950 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 147
ID ADC57304 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 148
ID ADC60495 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 149
ID ADC50970 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 150
ID ADC65497 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;

Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 151
ID ADC54595 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 152
ID ADC53556 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 153
ID ADC59079 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 154
ID ADC55957 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 155
ID ADC58527 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 156
ID ADC47198 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 157
ID ADD03201 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 158
ID ADC90193 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 159
ID ADC69612 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;

```
RESULT 160
ID ADC48501 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 161
ID ADD10030 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 162
ID ADC78073 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 163
ID ADD04605 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 164
ID ADD06308 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 165
ID ADC80561 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003052103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 166
ID ADD11068 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 167
ID ADD10345 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 168
ID ADC47949 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 169
ID ADC7827 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 170
ID ADC80009 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 171
ID ADD11305 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 172
ID ADD09478 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 173
ID ADD50790 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 174
ID ADD41191 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 175
ID ADD52330 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 176
ID ADD51036 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 177
ID ADD53070 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 178
ID ADD53622 standard; protein; 344 AA.
```

DE Novel human secreted and transmembrane protein PRO337.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 179
ID ADD37098 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 180
ID ADD51778 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 181
ID ADD02577 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 182
ID ADD0517 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 183
ID ADD02011 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 184
ID ADD54193 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 185
ID ADD50271 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 186
ID ADD51282 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 187
ID ADE49557 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.

PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 188
ID ADD92510 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 189
ID ADD91406 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 190
ID ADE04020 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 191
ID ADE32317 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 192
ID ADE22249 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 193
ID ADD79473 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 194
ID ADE35611 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 195
ID ADE16725 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 196
ID ADD73340 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203436-A1.

```
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 197
ID ADE42009 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 198
ID ADE17826 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 199
ID ADD91958 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 200
ID ADE33421 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 201
ID ADE33973 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 202
ID ADD80025 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 203
ID ADD93062 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 204
ID ADD72698 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 205
ID ADE19482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 206
ID ADE18930 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 207
ID ADE43126 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 208
ID ADD95915 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 209
ID ADE22801 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 210
ID ADD78919 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 211
ID ADE32869 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 212
ID ADE42561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 213
ID ADE17349 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 214
ID ADD80577 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
```


Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 215
ID ADG89605 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 216
ID ADE40889 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 217
ID ADE04688 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 218
ID ADE2817 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 219
ID ADF47363 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 220
ID ADG21526 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 221
ID ADG23167 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 222
ID ADF97502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 223
ID ADG80566 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 224
ID ADG53120 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 225
ID ADG60440 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 226
ID ADG80014 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 227
ID ADG63785 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 228
ID ADH55306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 229
ID ADH55858 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 230
ID ADI61200 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 231
ID ADI64077 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 232
ID ADI65026 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 233
ID ADG80566 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;

RESULT 233
ID ADI63525 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207387-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 234
ID ADH81939 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 235
ID ADH81387 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 236
ID ADM82556 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 237
ID ADN15955 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 238
ID ADN16584 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 239
ID ADN15403 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 240
ID ADN14851 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 241
ID ADC48829 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 242

ID ADC81113 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 243
ID ADE21000 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 244
ID ADE05844 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 245
ID ADD76561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 246
ID ADD75073 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 247
ID ADD75819 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 248
ID ADD85051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 249
ID ADD86877 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 250
ID ADE20754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 251
ID ADE39051 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 252
ID ADD87925 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 253
ID ADD86329 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 254
ID ADR05598 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 255
ID ADR73583 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 256
ID ADE75777 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 257
ID ADR48857 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 258
ID ADD78423 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 259
ID ADR41306 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 260
ID ADR23353 standard; protein; 344 AA.
DE Human PRO polypeptide #188.

PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 261
ID ADE21246 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 262
ID ADD77361 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 263
ID ADE20508 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 264
ID ADD75573 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 265
ID ADD74089 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 266
ID ADD74335 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 267
ID ADD76065 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 268
ID ADR85557 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 269
ID ADE23905 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092110-A1.

```

PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 270
ID ADE24548 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 271
ID ADD87373 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 272
ID ADE05106 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 273
ID ADD75319 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 274
ID ADD76863 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 275
ID ADD86631 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 276
ID ADE89239 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 277
ID ADE41199 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 278
ID ADD78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 279
ID ADE18378 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 280
ID ADE88687 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 281
ID ADE89958 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOIS/) BOISTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FIIV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 282
ID ADD77607 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 283
ID ADD77853 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 284
ID ADD85311 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100725-A1.

```

PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 285
 ID ADD73843 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100710-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 286
 ID ADD74581 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100713-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 287
 ID ADD77109 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100716-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 288
 ID ADD85803 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100720-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 289
 ID ADE05352 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100723-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 290
 ID ADD74827 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100724-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 291
 ID ADF61598 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003195345-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 292
 ID ADF40290 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003198994-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 293
 ID ADF46086 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003195148-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 294
 ID ADE94707 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003199027-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 295
 ID ADE91118 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003199061-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 296
 ID ADE95259 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003199052-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 297
 ID ADE93369 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003199060-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 298
 ID ADF24482 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003204055-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 299
 ID ADF40914 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003199021-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 300
 ID ADF23858 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003203402-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 301
 ID ADF33841 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003194780-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 5e-147;
 RESULT 302
 ID ADF34950 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003199029-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.

```
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 303
ID ADF27308 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 304
ID ADF27944 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 305
ID ADE92265 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 306
ID ADE90566 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 307
ID ADF41538 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 308
ID ADF33217 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 309
ID ADF25583 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 310
ID ADF26684 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 311
ID ADF34473 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 312
ID ADF46710 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 313
ID ADE91713 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 314
ID ADG05639 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 315
ID ADG27193 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 316
ID ADG02292 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 317
ID ADG22078 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 318
ID ADG20148 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 319
ID ADF98054 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 320
ID ADG24271 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
```

```
RESULT 321
ID ADF98625 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 322
ID ADG03456 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 323
ID ADF99177 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 324
ID ADG16762 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 325
ID ADG08221 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 326
ID ADG19488 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 327
ID ADG11256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 328
ID ADG13325 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 329
ID ADG08382 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 330
ID ADG07758 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 331
ID ADG12035 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 332
ID ADF96950 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 333
ID ADG06135 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 334
ID ADG23719 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 335
ID ADG04008 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 336
ID ADG24909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 337
ID ADF94592 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 338
ID ADG07206 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 339
ID ADG07758 standard; protein; 344 AA.
```

DE Novel human secreted and transmembrane protein PRO337.
PN US2003207356-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 340
ID ADG06688 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US200309666-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 341
ID ADG55253 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 342
ID ADG60917 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 343
ID ADG62021 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 344
ID ADG82222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 345
ID ADG57461 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 346
ID ADG56909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 347
ID ADG55805 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 348
ID ADG58565 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.

PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 349
ID ADG70931 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 350
ID ADH39032 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US200309665-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 351
ID ADG58013 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 352
ID ADG53597 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 353
ID ADG71483 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 354
ID ADG50696 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 355
ID ADG81670 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 356
ID ADH30632 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 357
ID ADG63634 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003180796-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 358
ID ADH11999 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 359
ID ADG50072 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 360
ID ADG51944 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 361
ID ADG52421 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 362
ID ADG54149 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 363
ID ADG49448 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 364
ID ADG81118 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 365
ID ADG56357 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 366
ID ADH12623 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 367
ID ADG48824 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 368
ID ADG61469 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 369
ID ADH28556 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 370
ID ADG54701 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 371
ID ADG59741 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 372
ID ADG51320 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 373
ID ADH43489 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 374
ID ADG59264 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 375
ID ADG34122 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;

```
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 376
ID ADG62720 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 377
ID ADI18165 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 378
ID ADI33592 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 379
ID ADH69686 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 380
ID ADH25745 standard; protein; 344 AA.
DE Human PRO337 protein SEQ ID NO:523.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 381
ID ADG09908 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 382
ID ADI15379 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 383
ID ADG09256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 384
ID ADI14711 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 385
ID ADI29847 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 386
ID ADI18306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 387
ID ADM27244 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 388
ID ADJ63587 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 389
ID ADJ77482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 390
ID ADK82834 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 391
ID ADK66602 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 392
ID ADJ65604 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 393
ID ADM27740 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 394
ID ADM27740 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 394
```

```
ID ADM17522 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 395
ID ADL07356 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 396
ID ADM42464 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 397
ID ADM28326 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 398
ID ADI95808 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 399
ID ADI96360 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 400
ID ADS32312 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 401
ID ADT03296 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 402
ID ADU50478 standard; protein; 344 AA.
DE PRO337, SEQ ID 523.
PN US2004223964-A1.
PD 11-NOV-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;
RESULT 403
ID ADW49757 standard; protein; 344 AA.
DE PRO337 protein, SEQ ID 523.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 9; Length 344;
RESULT 404
ID ADZ03347 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO337 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 9; Length 344;
RESULT 405
ID ADZ52418 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 9; Length 344;
```

```
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 406
ID AEB14093 standard; protein; 344 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 376.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 1806; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e-147;
RESULT 407
ID AAM40499 standard; protein; 355 AA.
DE Human polypeptide SEQ ID NO 5430.
PN WO2001533112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1806; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.2e-147;
RESULT 408
ID ADI21580 standard; protein; 355 AA.
DE Novel human polypeptide #59.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1806; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.2e-147;
RESULT 409
ID AAB19722 standard; protein; 344 AA.
DE Human SECX Clone 11753149.0.37-encoded protein.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 3; Length 344;
Best Local Similarity 99.7%; Pred. No. 2e-146;
RESULT 410
ID AAB19721 standard; protein; 344 AA.
DE Human SECX Clone 11753149.0.6-encoded protein.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 3; Length 344;
Best Local Similarity 99.7%; Pred. No. 2e-146;
RESULT 411
ID ADD18291 standard; protein; 344 AA.
DE Human molecule (MOL) protein MOLI1.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 7; Length 344;
Best Local Similarity 99.7%; Pred. No. 2e-146;
RESULT 412
ID ADD18289 standard; protein; 344 AA.
DE Human molecule (MOL) protein MOLI0.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.6%; Score 1799; DB 7; Length 344;
Best Local Similarity 99.7%; Pred. No. 2e-146;
RESULT 413
ID AAY41773 standard; protein; 343 AA.
DE Human PRO337 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Query Match 99.2%; Score 1791.5; DB 2; Length 343;
Best Local Similarity 99.7%; Pred. No. 8.9e-146;
RESULT 414
ID AAM38713 standard; protein; 344 AA.
DE Human polypeptide SEQ ID NO 1858.
PN WO2001533112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 92.2%; Score 1665.5; DB 4; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.6e-135;
RESULT 415
ID ABJ20227 standard; protein; 344 AA.
DE Human IG gene related protein SEQ ID NO 50.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 92.2%; Score 1665.5; DB 6; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.6e-135;
RESULT 416
ID ABUS6719 standard; protein; 344 AA.
DE Lung cancer-associated polypeptide #312.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 92.2%; Score 1665.5; DB 6; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.6e-135;
RESULT 417
ID ADG63209 standard; protein; 344 AA.
DE Human neurotrimin protein.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 92.2%; Score 1665.5; DB 7; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.6e-135;
RESULT 418
ID ADN39138 standard; protein; 344 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:456.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 92.2%; Score 1665.5; DB 7; Length 344;
Best Local Similarity 95.2%; Pred. No. 6.6e-135;
RESULT 419
ID ADG63211 standard; protein; 355 AA.
DE Human neurotrimin protein +33bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 91.4%; Score 1850; DB 7; Length 355;
Best Local Similarity 92.2%; Pred. No. 1.5e-133;
RESULT 420
ID ADI35770 standard; protein; 355 AA.
DE Human neurotrimin.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 91.4%; Score 1650; DB 7; Length 355;
Best Local Similarity 92.2%; Pred. No. 1.5e-133;
RESULT 421
ID ADG63213 standard; protein; 367 AA.
DE Human neurotrimin protein +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 91.0%; Score 1644; DB 7; Length 367;
Best Local Similarity 89.1%; Pred. No. 5.1e-133;
RESULT 422
```

ID AAV79205 standard; protein; 381 AA.
DE Human Kruppel associated DNA binding protein 42.
PN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.
Query Match 91.0%; Score 1643; DB 5; Length 381;
Best Local Similarity 98.7%; Pred. No. 6.6e-133;
RESULT 423
ID AAV57602 standard; protein; 313 AA.
DE Human protein SEQ ID NO:4.
PN WO9958668-A1.
PD 18-NOV-1999.
PA (ONNOY) ONO PHARM CO LTD.
Query Match 90.9%; Score 1642; DB 3; Length 313;
Best Local Similarity 100.0%; Pred. No. 6.1e-133;
RESULT 424
ID ADI35772 standard; protein; 344 AA.
DE Rat neurotrophin.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 90.8%; Score 1639.5; DB 7; Length 344;
Best Local Similarity 92.9%; Pred. No. 1.1e-132;
RESULT 425
ID ADG63215 standard; protein; 376 AA.
DE Human neurotrophin protein +108bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 90.8%; Score 1639.5; DB 7; Length 376;
Best Local Similarity 87.0%; Pred. No. 1.3e-132;
RESULT 426
ID ABE07928 standard; protein; 338 AA.
DE Novel protein (useful for identifying genetic disorders) #83.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 71.7%; Score 1295.5; DB 7; Length 338;
Best Local Similarity 71.6%; Pred. No. 5.3e-103;
RESULT 427
ID ADO47380 standard; protein; 250 AA.
DE Human neurotrophin-like protein-related rat neurotrophin protein SeqID15.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NOVE-) NOVELO.
Query Match 71.7%; Score 1295; DB 8; Length 250;
Best Local Similarity 97.6%; Pred. No. 3.8e-103;
RESULT 428
ID ABJ20236 standard; protein; 345 AA.
DE Human IG gene related protein SEQ ID No 59.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 70.2%; Score 1268; DB 6; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 429
ID ABE83448 standard; protein; 345 AA.
DE Human Protein Q14982, SEQ ID NO 11043.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 70.2%; Score 1268; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 430
ID ADG63207 standard; protein; 345 AA.
DE Opioid-binding protein/cell adhesion molecule-like protein.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 70.2%; Score 1268; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 431

ID ADV73205 standard; protein; 345 AA.
DE Human colon tumor cell upregulated protein SEQ ID NO 46.
PN WO2004110345-A2.
PD 23-DEC-2004.
PA (PHAA) PHARMACIA CORP.
Query Match 70.2%; Score 1268; DB 9; Length 345;
Best Local Similarity 71.2%; Pred. No. 1.3e-100;
RESULT 432
ID ADE83446 standard; protein; 345 AA.
DE Rat Protein P32736, SEQ ID NO 11041.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 69.7%; Score 1259; DB 7; Length 345;
Best Local Similarity 71.2%; Pred. No. 7.6e-100;
RESULT 433
ID AAO19641 standard; protein; 335 AA.
DE Human limbic system associated membrane protein 36-85.
PN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.
Query Match 51.8%; Score 932.5; DB 5; Length 335;
Best Local Similarity 53.9%; Pred. No. 1.1e-71;
RESULT 434
ID ABJ20235 standard; protein; 338 AA.
DE Human IG gene related protein SEQ ID No 58.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 51.6%; Score 931.5; DB 6; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.3e-71;
RESULT 435
ID ADL1675 standard; protein; 338 AA.
DE Human steroid-induced C3A liver cell protein #60.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 51.6%; Score 931.5; DB 8; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.3e-71;
RESULT 436
ID ADX26265 standard; protein; 338 AA.
DE Novel cell pain response detection method-related human protein SeqID611.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 51.6%; Score 931.5; DB 9; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.3e-71;
RESULT 437
ID AAW05153 standard; protein; 338 AA.
DE Rat LAMP residues 1-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.5e-71;
RESULT 438
ID AAW05154 standard; protein; 338 AA.
DE Rat LAMP residues 1-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.5e-71;
RESULT 439
ID ADX26409 standard; protein; 338 AA.
DE Novel cell pain response detection method-related rat protein SeqID755.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 51.3%; Score 926.5; DB 9; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.5e-71;
RESULT 440

ID AEA26105 standard; protein; 334 AA.
DE Human renal cell carcinoma-related LSAMP protein SeqID125.
PN WO2005047519-A2.
PD 26-MAY-2005.
PA (VAND-) VAN ANDEL RES INST.
Query Match 51.2%; Score 925.5; DB 9; Length 334;
Best Local Similarity 55.3%; Pred. No. 4.3e-71;
RESULT 441
ID AAW05152 standard; protein; 325 AA.
DE Human LAMP residues 8-332.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.1e-71;
RESULT 442
ID AAW05172 standard; protein; 361 AA.
DE Rat LAMP clone 6C.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.8%; Score 913; DB 2; Length 361;
Best Local Similarity 51.7%; Pred. No. 5.7e-70;
RESULT 443
ID AAW05157 standard; protein; 308 AA.
DE Human LAMP residues 8-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.3%; Score 908; DB 2; Length 308;
Best Local Similarity 56.3%; Pred. No. 1.2e-69;
RESULT 444
ID AAW05158 standard; protein; 315 AA.
DE Rat LAMP residues 1-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.2%; Score 907; DB 2; Length 315;
Best Local Similarity 56.3%; Pred. No. 1.5e-69;
RESULT 445
ID AAW05156 standard; protein; 310 AA.
DE Rat mature LAMP.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 50.1%; Score 905; DB 2; Length 310;
Best Local Similarity 55.3%; Pred. No. 2.3e-69;
RESULT 446
ID AAW05155 standard; protein; 304 AA.
DE Human mature LAMP.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.9%; Score 902; DB 2; Length 304;
Best Local Similarity 55.5%; Pred. No. 4e-69;
RESULT 447
ID ADX26335 standard; protein; 341 AA.
DE Novel cell pain response detection method-related mouse protein SeqID681.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 49.5%; Score 894; DB 9; Length 341;
Best Local Similarity 56.3%; Pred. No. 2.3e-68;
RESULT 448
ID ABR39441 standard; protein; 383 AA.
DE Human GENSET polypeptide clone name SLAMP.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GENT) GENSET SA.
Query Match 49.4%; Score 893; DB 6; Length 383;
Best Local Similarity 53.3%; Pred. No. 3.3e-68;
RESULT 449
ID AAW05159 standard; protein; 287 AA.

DE Human LAMP residues 29-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.1%; Score 886.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 8e-68;
RESULT 450
ID AAW05160 standard; protein; 287 AA.
DE Rat LAMP residues 29-315.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 49.0%; Score 885.5; DB 2; Length 287;
Best Local Similarity 56.6%; Pred. No. 9.8e-68;
RESULT 451
ID ADM47275 standard; protein; 203 AA.
DE Oestrogen regulated protein like NOVX 25b protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 48.4%; Score 873.5; DB 7; Length 203;
Best Local Similarity 54.5%; Pred. No. 6.6e-67;
RESULT 452
ID AAG75020 standard; protein; 326 AA.
DE Human colon cancer antigen protein SEQ ID NO:5784.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 47.2%; Score 852.5; DB 4; Length 326;
Best Local Similarity 51.6%; Pred. No. 8.2e-65;
RESULT 453
ID AAB31212 standard; protein; 354 AA.
DE Amino acid sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 4; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 454
ID ABP53580 standard; protein; 354 AA.
DE Human NOV12a protein SEQ ID NO:24.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 455
ID AAU83592 standard; protein; 354 AA.
DE Human PRO protein, Seq ID No 2.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 456
ID ADI28023 standard; protein; 354 AA.
DE ECMCAD protein 7087904CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCV-) INCVTE GENOMICS INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 457
ID ADY31742 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 458
ID ABU80739 standard; protein; 354 AA.
DE Human PRO polypeptide #1.

PN US2003036635-A1.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 459
ID ABO25183 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 460
ID ABO33705 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 461
ID ABU67301 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 462
ID ABU72069 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200217165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 463
ID ABU67170 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 464
ID ABU82048 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 465
ID ABU79812 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 466
ID ABU72228 standard; protein; 354 AA.
DE Human PRO6004 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 467
ID ADA47302 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003044844-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 468
ID ABJ72356 standard; protein; 354 AA.
DE Human PRO6004 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 469
ID ABO34251 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO 6004.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 470
ID ABO19870 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 471
ID ABJ72058 standard; protein; 354 AA.
DE Human membrane bound receptor/protein PRO6004 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 472
ID ADB83492 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 473
ID ADB80598 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 474
ID ADB73139 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 475
ID ADB78221 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 476
ID ADB84869 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003073817-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 477
ID ADB775975 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 478
ID ADB87041 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
FN US2003088067-A1;
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 479
ID ADB84623 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
FN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 480
ID ADB83738 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 481
ID ADB72893 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 482
ID ADC36731 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
FN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 483
ID ADC21721 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
FN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 484
ID ADC49752 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 485
ID ADC48951 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 486
ID ADC49468 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 487
ID ADC47329 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 488
ID ADC47074 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 489
ID ADC77949 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 490
ID AD060184 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 491
ID ADC77703 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 492
ID AD050666 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 493
ID AD050912 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
FN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 494
ID AD050393 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
FN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 495
ID AD050393 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
FN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;


```
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 495
ID ADD50147 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 496
ID ADS15158 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 497
ID ADG63811 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 498
ID ADC48705 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 499
ID ADE20876 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 500
ID ADE05720 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 501
ID ADD74949 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 502
ID ADD75695 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 503
ID ADD84927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 504
ID ADD86753 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 505
ID ADE20630 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 506
ID ADE38927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 507
ID ADE05474 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 508
ID ADD73459 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 509
ID ADD78299 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 510
ID ADE21122 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 511
ID ADD77237 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 512
ID ADE20384 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 513
ID ADE20384 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
```

```
ID ADD75449 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 514
ID ADD73965 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 515
ID ADD74211 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 516
ID ADD75941 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 517
ID ADD85433 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 518
ID ADE04982 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 519
ID ADD75195 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 520
ID ADD76739 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 521
ID ADD86507 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 522
ID ADE41225 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 523
ID ADD77975 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 524
ID ADD77483 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 525
ID ADD77729 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 526
ID ADD85187 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 527
ID ADD73719 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 528
ID ADD74457 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 529
ID ADD76985 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 530
ID ADD85679 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 531
ID ADE05228 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
```

```
PN US2003100723-A1.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 532
ID ADD74703 standard;|protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 533
ID ADG05515 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 534
ID ADG27069 standard;|protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 535
ID ADG11132 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 536
ID ADG11911 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 537
ID ADF94468 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 538
ID ADG06564 standard;|protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 539
ID ADH38908 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 540
ID ADG63659 standard;|protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003180796-A1.

PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 541
ID ADG33998 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 542
ID ADI33468 standard;|protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 543
ID ADH69562 standard;|protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 544
ID ADI29723 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 545
ID ADM27120 standard;|protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 546
ID ADK66478 standard;|protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 547
ID ADS82050 standard;|protein; 354 AA.
DE Human cancer-associated protein #5.
PN WQ2004035789-A1.
PD 23-APR-2004.
PA (GLDS ) LG LIFE SCI LTD.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.2e-62;
RESULT 548
ID ABB98407 standard;|protein; 354 AA.
DE Human NOV6, KILON-like protein.
PN WQ200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.5%; Score 822; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.9e-62;
RESULT 549
ID ADB64811 standard;|protein; 354 AA.
DE Human protein encoded by clone OCBBF20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
```

PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 45.4%; Score 820; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 5.8e-62;
RESULT 550
ID ABP53581 standard; protein; 354 AA.
DE Human NOV12b protein SEQ ID NO:26.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.3%; Score 819; DB 5; Length 354;
Best Local Similarity 48.6%; Pred. No. 7.1e-62;
RESULT 551
ID ABJ20234 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO 57.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.5e-61;
RESULT 552
ID ABJ20233 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO 56.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.5e-61;
RESULT 553
ID AAB44331 standard; protein; 352 AA.
DE Human PRO4993 protein sequence SEQ ID NO:612.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 3; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 554
ID ABO25277 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 555
ID ABU72283 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 556
ID ABU09489 standard; protein; 352 AA.
DE Human secreted and transmembrane PRO polypeptide #39.
PN US200217753-A1.
PD 28-NOV-2002.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 557
ID ABU61161 standard; protein; 352 AA.
DE Human PRO4993 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 558
ID ABU80430 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PD 02-JAN-2003.

PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 559
ID ADA25150 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 560
ID ABO19732 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 561
ID ADA12812 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO4993.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 562
ID ABO19623 standard; protein; 352 AA.
DE Novel human secreted and transmembrane polypeptide #91.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 563
ID ADB74118 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 564
ID ADB76834 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 565
ID ADC44260 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 566
ID ADC62020 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003049884-A1.
PD 13-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 567
ID ADC63984 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;

```
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 568
ID ADC67084 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 569
ID ADC69208 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 570
ID ADC63268 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 571
ID ADC68333 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 572
ID ADC41653 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 573
ID ADC67708 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 574
ID ADC62644 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 575
ID ADC42277 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 576
ID ADE49646 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 577
ID ADE35700 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 578
ID ADE16814 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 579
ID ADD73429 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 580
ID ADD72787 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 581
ID ADE17438 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 582
ID ADF47452 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 583
ID ADG53209 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 584
ID ADG60529 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 585
ID ADI61289 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 586
```

ID ADE48946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 587
ID ADE90047 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYN/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 588
ID ADF61687 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 589
ID ADF40379 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 590
ID ADF46175 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 591
ID ADF24571 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 592
ID ADF41003 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 593
ID ADF23947 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 594
ID ADF33930 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 595
ID ADF27397 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 596
ID ADF28033 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 597
ID ADF41627 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 598
ID ADF33306 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 599
ID ADF25672 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 600
ID ADF26773 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 601
ID ADF26773 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;

ID ADF34562 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 602
ID ADF46799 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 603
ID ADG50785 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 604
ID ADG50161 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 605
ID ADG52033 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 606
ID ADG49537 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 607
ID ADG48913 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003218560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 608
ID ADG51409 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 609
ID ADG59353 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 610
ID ADG62809 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 611
ID ADM17611 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 612
ID ADL07445 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 613
ID ADU50567 standard;|protein; 352 AA.
DE PRO4993, SEQ ID 612.
PN US2004223964-A1.
PD 11-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 614
ID ADW49846 standard;|protein; 352 AA.
DE PRO4993 protein, SEQ ID 612.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.1%; Score 815; DB 9; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.6e-61;
RESULT 615
ID ABZ52507 standard;|protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.

PA (EATO/) EATON D L.
 PA (FER/) FERRARA N.
 PA (FIL/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GER/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI J C.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (KUOS/) KUO S S.
 PA (NAPI/) NAPIER M A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (SHEL/) SHELTON D L.
 PA (STEW/) STEWART T A.
 PA (TUNA/) TUNAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 45.1%; Score 815; DB 9; Length 352;
 Best Local Similarity 47.5%; Pred. No. 1.6e-61;
 RESULT 616
 ID AAW05167 standard; protein; 252 AA.
 DE Human LAMP residues 46-294.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 44.1%; Score 796.5; DB 2; Length 252;
 Best Local Similarity 56.9%; Pred. No. 3.9e-60;
 RESULT 617
 ID AAW05168 standard; protein; 252 AA.
 DE Rat LAMP residues 46-294.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 44.0%; Score 795.5; DB 2; Length 252;
 Best Local Similarity 56.9%; Pred. No. 4.7e-60;
 RESULT 618
 ID ABG96271 standard; protein; 336 AA.
 DE Human immunoglobulin superfamily protein IGSFP-9.
 PN WO200272794-A2.
 PD 19-SEP-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 42.2%; Score 763; DB 5; Length 336;
 Best Local Similarity 50.6%; Pred. No. 4.5e-57;
 RESULT 619
 ID AAE29924 standard; protein; 336 AA.
 DE Human LP289 protein.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 42.2%; Score 763; DB 6; Length 336;
 Best Local Similarity 50.8%; Pred. No. 4.5e-57;
 RESULT 620
 ID ADH71418 standard; protein; 336 AA.
 DE Human protein of the invention NOV11q SEQ ID NO:314.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.2%; Score 763; DB 8; Length 336;
 Best Local Similarity 50.6%; Pred. No. 4.5e-57;
 RESULT 621
 ID ADH71412 standard; protein; 336 AA.
 DE Human protein of the invention NOV1ln SEQ ID NO:308.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.2%; Score 763; DB 8; Length 336;
 Best Local Similarity 50.6%; Pred. No. 4.5e-57;
 RESULT 622
 ID ADH71414 standard; protein; 336 AA.
 DE Human protein of the invention NOV1lo SEQ ID NO:310.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.2%; Score 763; DB 8; Length 336;
 Best Local Similarity 50.6%; Pred. No. 4.5e-57;
 RESULT 623
 ID ADH71388 standard; protein; 344 AA.
 DE Human protein of the invention NOV1lb SEQ ID NO:284.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.2%; Score 763; DB 8; Length 344;
 Best Local Similarity 50.6%; Pred. No. 4.6e-57;
 RESULT 624
 ID ADH71390 standard; protein; 325 AA.
 DE Human protein of the invention NOV1lc SEQ ID NO:286.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.2%; Score 762; DB 8; Length 325;
 Best Local Similarity 50.5%; Pred. No. 5.2e-57;
 RESULT 625
 ID AAE30252 standard; protein; 306 AA.
 DE Human LP289 mature protein #1.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 42.1%; Score 761; DB 6; Length 306;
 Best Local Similarity 52.5%; Pred. No. 5.8e-57;
 RESULT 626
 ID ADH71402 standard; protein; 307 AA.
 DE Human protein of the invention NOV1li SEQ ID NO:298.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 307;
 Best Local Similarity 52.5%; Pred. No. 5.9e-57;
 RESULT 627
 ID ADH71410 standard; protein; 309 AA.
 DE Human protein of the invention NOV1lm SEQ ID NO:306.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 309;
 Best Local Similarity 52.5%; Pred. No. 5.9e-57;
 RESULT 628
 ID ADH71406 standard; protein; 309 AA.
 DE Human protein of the invention NOV1lk SEQ ID NO:302.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 309;
 Best Local Similarity 52.5%; Pred. No. 5.9e-57;
 RESULT 629
 ID AAE30253 standard; protein; 314 AA.
 DE Human LP289 mature protein #2.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 42.1%; Score 761; DB 6; Length 314;
 Best Local Similarity 52.5%; Pred. No. 6e-57;
 RESULT 630
 ID ADH71394 standard; protein; 315 AA.
 DE Human protein of the invention NOV1le SEQ ID NO:290.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 315;
 Best Local Similarity 52.5%; Pred. No. 6.1e-57;
 RESULT 631

ID ABG94637 standard; protein; 319 AA.
DE Human NOV5b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 5; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 632
ID ABG94636 standard; protein; 319 AA.
DE Human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 5; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 633
ID ADL35977 standard; protein; 319 AA.
DE Human NOVX polypeptide #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 42.1%; Score 761; DB 7; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 634
ID ADL35979 standard; protein; 319 AA.
DE Human NOVX polypeptide #12.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 42.1%; Score 761; DB 7; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 635
ID ADH71400 standard; protein; 319 AA.
DE Human protein of the invention NOV11h SEQ ID NO:296.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 636
ID ADH71396 standard; protein; 319 AA.
DE Human protein of the invention NOV11f SEQ ID NO:292.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 319;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 637
ID ADH71416 standard; protein; 320 AA.
DE Human protein of the invention NOV11p SEQ ID NO:312.
PN WO2003102155-A2.

PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 320;
Best Local Similarity 52.5%; Pred. No. 6.2e-57;
RESULT 638
ID ADH71398 standard; protein; 325 AA.
DE Human protein of the invention NOV11g SEQ ID NO:294.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 761; DB 8; Length 325;
Best Local Similarity 52.5%; Pred. No. 6.3e-57;
RESULT 639
ID ADH71422 standard; protein; 336 AA.
DE Human protein of the invention NOV11s SEQ ID NO:318.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 760; DB 8; Length 336;
Best Local Similarity 50.6%; Pred. No. 8.1e-57;
RESULT 640
ID ADH71386 standard; protein; 336 AA.
DE Human protein of the invention NOV11a SEQ ID NO:282.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 42.1%; Score 760; DB 8; Length 336;
Best Local Similarity 50.8%; Pred. No. 8.1e-57;
RESULT 641
ID ABG94638 standard; protein; 307 AA.
DE Human NOV5c protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 5; Length 307;
Best Local Similarity 52.5%; Pred. No. 1.3e-56;
RESULT 642
ID ADH71404 standard; protein; 319 AA.
DE Human protein of the invention NOV11j SEQ ID NO:300.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 8; Length 319;
Best Local Similarity 52.5%; Pred. No. 1.4e-56;
RESULT 643
ID ADH71420 standard; protein; 336 AA.
DE Human protein of the invention NOV11r SEQ ID NO:316.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 8; Length 336;
Best Local Similarity 50.3%; Pred. No. 1.5e-56;
RESULT 644
ID ADP29916 standard; protein; 278 AA.
DE Human secreted protein SEQ ID #683.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 41.7%; Score 752.5; DB 8; Length 278;
Best Local Similarity 54.1%; Pred. No. 2.8e-56;
RESULT 645
ID AAE30254 standard; protein; 284 AA.
DE Human LP289 mature protein #3.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 284;
Best Local Similarity 54.1%; Pred. No. 2.8e-56;
RESULT 646
ID AAE30256 standard; protein; 291 AA.
DE Human LP289 mature protein #5.
PN WO200274906-A2.
PD 26-SEP-2002.

```
PA (ELIL ) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 291;
Best Local Similarity 54.1%; Pred. No. 2.9e-56;
RESULT 647
ID AAE30255 standard; protein; 292 AA.
DE Human LP289 mature protein #4.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 292;
Best Local Similarity 54.1%; Pred. No. 3e-56;
RESULT 648
ID ADL35981 standard; protein; 305 AA.
DE Human NOVX polypeptide #13.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 39.4%; Score 712; DB 7; Length 336;
Best Local Similarity 50.2%; Pred. No. 1.1e-52;
RESULT 655
ID ADH71392 standard; protein; 253 AA.
DE Human protein of the invention NOV11d SEQ ID NO:288.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.1%; Score 687.5; DB 8; Length 253;
Best Local Similarity 55.6%; Pred. No. 9.8e-51;
RESULT 656
ID AAU84385 standard; protein; 351 AA.
DE Novel human secreted or membrane-associated protein #24.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (GLAX ) GLAXO GROUP LTD.
Query Match 37.7%; Score 681.5; DB 5; Length 351;
Best Local Similarity 50.7%; Pred. No. 5.1e-50;
RESULT 657
ID ABG13848 standard; protein; 141 AA.
DE Novel human diagnostic protein #13839.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 33.4%; Score 603; DB 4; Length 141;
Best Local Similarity 86.6%; Pred. No. 8.6e-44;
RESULT 658
ID AAE30271 standard; protein; 294 AA.
DE Human LP319b protein variant #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 33.4%; Score 603; DB 6; Length 294;
Best Local Similarity 45.0%; Pred. No. 2.3e-43;
RESULT 659
ID AAE30270 standard; protein; 286 AA.
DE Human LP319b protein variant #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 33.2%; Score 600; DB 6; Length 286;
Best Local Similarity 45.0%; Pred. No. 4.1e-43;
RESULT 660
ID ADP29917 standard; protein; 222 AA.
DE Human secreted protein SEQ ID #684.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 33.2%; Score 599.5; DB 8; Length 222;
Best Local Similarity 54.0%; Pred. No. 3.2e-43;
RESULT 661
ID ABG13847 standard; protein; 130 AA.
DE Novel human diagnostic protein #13838.
```

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 31.5%; Score 569.5; DB 4; Length 130;
Query Match 88.9%; Pred. No. 6e-41;
Best Local Similarity 31.5%; Score 569.5; DB 4; Length 130;
RESULT 662
ID AAE30269 standard; protein; 234 AA.
DE Human LP319b protein mature sequence #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI. 29.2%; Score 527; DB 6; Length 234;
Query Match 53.2%; Pred. No. 6.2e-37;
Best Local Similarity 29.2%; Score 527; DB 6; Length 234;
RESULT 663
ID AAE29927 standard; protein; 256 AA.
DE Human LP319b protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI. 29.2%; Score 527; DB 6; Length 256;
Query Match 53.2%; Pred. No. 7e-37;
Best Local Similarity 29.2%; Score 527; DB 6; Length 256;
RESULT 664
ID AEG13816 standard; protein; 872 AA.
DE Novel human diagnostic protein #13807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 29.1%; Score 525.5; DB 4; Length 872;
Query Match 43.4%; Pred. No. 5e-36;
Best Local Similarity 29.1%; Score 525.5; DB 4; Length 872;
RESULT 665
ID ADE08994 standard; protein; 872 AA.
DE Novel protein-related contig polypeptide sequence #60.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC. 29.1%; Score 525.5; DB 7; Length 872;
Query Match 43.4%; Pred. No. 5e-36;
Best Local Similarity 29.1%; Score 525.5; DB 7; Length 872;
RESULT 666
ID AAE30268 standard; protein; 226 AA.
DE Human LP319b protein mature sequence #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI. 28.0%; Score 505; DB 6; Length 226;
Query Match 53.0%; Pred. No. 4.6e-35;
Best Local Similarity 28.0%; Score 505; DB 6; Length 226;
RESULT 667
ID AAE30264 standard; protein; 211 AA.
DE Human LP319a protein mature sequence #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI. 26.1%; Score 472; DB 6; Length 211;
Query Match 54.1%; Pred. No. 3e-32;
Best Local Similarity 26.1%; Score 472; DB 6; Length 211;
RESULT 668
ID AAE30265 standard; protein; 222 AA.
DE Human LP319a protein mature sequence #2.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI. 26.1%; Score 472; DB 6; Length 222;
Query Match 54.1%; Pred. No. 3.2e-32;
Best Local Similarity 26.1%; Score 472; DB 6; Length 222;
RESULT 669
ID AAE29926 standard; protein; 241 AA.
DE Human LP319a protein.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI. 26.1%; Score 472; DB 6; Length 241;
Query Match 54.1%; Pred. No. 3.6e-32;
Best Local Similarity 26.1%; Score 472; DB 6; Length 241;
RESULT 670
ID ABE69485 standard; protein; 413 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35247.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 18.7%; Score 338.5; DB 4; Length 413;
Query Match 28.0%; Pred. No. 2.4e-20;
Best Local Similarity 18.7%; Score 338.5; DB 4; Length 413;
RESULT 671
ID ABB65642 standard; protein; 315 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23718.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 18.4%; Score 333; DB 4; Length 315;
Query Match 31.9%; Pred. No. 5e-20;
Best Local Similarity 18.4%; Score 333; DB 4; Length 315;
RESULT 672
ID ABB62574 standard; protein; 545 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14514.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 16.9%; Score 306; DB 4; Length 545;
Query Match 28.9%; Pred. No. 2.3e-17;
Best Local Similarity 16.9%; Score 306; DB 4; Length 545;
RESULT 673
ID ABB58947 standard; protein; 333 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3633.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 16.5%; Score 297.5; DB 4; Length 333;
Query Match 29.7%; Pred. No. 6.2e-17;
Best Local Similarity 16.5%; Score 297.5; DB 4; Length 333;
RESULT 674
ID ADS10483 standard; protein; 2537 AA.
DE Human therapeutic protein - SEQ ID 720.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC. 16.1%; Score 290.5; DB 8; Length 2537;
Query Match 29.8%; Pred. No. 4e-15;
Best Local Similarity 16.1%; Score 290.5; DB 8; Length 2537;
RESULT 675
ID ADS98860 standard; protein; 2537 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1124.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T. 16.1%; Score 290.5; DB 8; Length 2537;
Query Match 29.8%; Pred. No. 4e-15;
Best Local Similarity 16.1%; Score 290.5; DB 8; Length 2537;
RESULT 676
ID ABEU12083 standard; protein; 2572 AA.
DE Human NOV25b CG93858-02 protein SEQ ID 86.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP. 16.1%; Score 290.5; DB 6; Length 2572;
Query Match 29.8%; Pred. No. 4.1e-15;
Best Local Similarity 16.1%; Score 290.5; DB 6; Length 2572;
RESULT 677
ID ADK60225 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S. 16.1%; Score 290.5; DB 8; Length 2673;
Query Match 29.8%; Pred. No. 4.3e-15;
Best Local Similarity 16.1%; Score 290.5; DB 8; Length 2673;
RESULT 678
ID ADK60526 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S. 16.1%; Score 290.5; DB 8; Length 2673;
Query Match 29.8%; Pred. No. 4.3e-15;
Best Local Similarity 16.1%; Score 290.5; DB 8; Length 2673;
RESULT 679
ID ADP73149 standard; protein; 2673 AA.

DE Angiogenesis inhibitor human protein sequence, GS-P52.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 4.3e-15;
RESULT 680
ID ABU89135 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 4495;
Best Local Similarity 29.8%; Pred. No. 8.8e-15;
RESULT 681
ID ADH72106 standard; protein; 4495 AA.
DE Human protein of the invention NOVA3c SEQ ID NO:1002.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 8.8e-15;
RESULT 682
ID ADO08273 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASH/) CASHMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KERUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERHUSEN B D.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 8.8e-15;
RESULT 683
ID ADJ70089 standard; protein; 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1895.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
RESULT 684
ID ADJ8137 standard; protein; 5636 AA.
DE Human hemicentin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHER/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASH/) CASHMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
RESULT 685
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
RESULT 686
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
RESULT 687
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
RESULT 688
ID ADG39844 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #5.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KERUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.

PA (KOMU/) KOMUVES L.
Query Match 16.0%; Score 289.5; DB 7; Length 1708;
Best Local Similarity 29.8%; Pred. No. 2.9e-15;
RESULT 689
ID ADG39840 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #1.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHINKETS R A.
PA (PADL/) PADIGARU M.
PA (KERU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER T N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 16.0%; Score 289.5; DB 7; Length 1708;
Best Local Similarity 31.1%; Pred. No. 2.9e-15;
RESULT 690
ID ABU69134 standard; protein; 707 AA.
DE Human NOVX polypeptide #9.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 6; Length 707;
Best Local Similarity 31.1%; Pred. No. 1e-15;
RESULT 691
ID ADH72102 standard; protein; 707 AA.
DE Human protein of the invention NOV43a SEQ ID NO:998.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 8; Length 707;
Best Local Similarity 31.1%; Pred. No. 1e-15;
RESULT 692
ID ADO08271 standard; protein; 707 AA.
DE Human NOVX polypeptide #9.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASW/) CASHMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADL/) PADIGARU M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHINKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.

PA (ZERH/) ZERHUSEN B D.
Query Match 16.0%; Score 288.5; DB 8; Length 707;
Best Local Similarity 31.1%; Pred. No. 1e-15;
RESULT 693
ID ADH72104 standard; protein; 712 AA.
DE Human protein of the invention NOV43b SEQ ID NO:1000.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 8; Length 712;
Best Local Similarity 31.1%; Pred. No. 1.1e-15;
RESULT 694
ID ABU99129 standard; protein; 961 AA.
DE Novel human GPCR related protein NOV9b.
PN WO200299116-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 6; Length 961;
Best Local Similarity 30.5%; Pred. No. 1.6e-15;
RESULT 695
ID ADM93823 standard; protein; 961 AA.
DE Human NOV protein #21.
PN US2004009480-A1.
PD 15-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (BAUM/) BAUMGARTNER J C.
PA (BOLD/) BOLDOG F L.
PA (CASW/) CASHMAN S J.
PA (EDIN/) EDINGER S R.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X S.
PA (HJAL/) HJALT T.
PA (KEKU/) KEKUDA R.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PADL/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHINKETS R A.
PA (STON/) STONE D J.
PA (SPYT/) SPYTEK K A.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 16.0%; Score 288.5; DB 8; Length 961;
Best Local Similarity 30.5%; Pred. No. 1.6e-15;
RESULT 696
ID ABG03933 standard; protein; 1240 AA.
DE Novel human diagnostic protein #3924.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.0%; Score 288.5; DB 4; Length 1240;
Best Local Similarity 31.1%; Pred. No. 2.3e-15;
RESULT 697
ID AAB47771 standard; protein; 1336 AA.
DE Human thrombospondin protein, BTL.012.
PN WO200174852-A2.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Query Match 16.0%; Score 288.5; DB 5; Length 1336;
Best Local Similarity 31.1%; Pred. No. 2.5e-15;
RESULT 698
ID ABU12084 standard; protein; 1902 AA.
DE Human NOV25c CG56914-03 protein SEQ ID 88.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.

Query Match 16.0%; Score 288.5; DB 6; Length 1902;
Best Local Similarity 31.1%; Pred. No. 4e-15;
RESULT 699
ID ADH72108 standard; protein; 1902 AA.
DE Human protein of the invention NOV43d SEQ ID NO:1004.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 8; Length 1902;
Best Local Similarity 31.1%; Pred. No. 4e-15;
RESULT 700
ID ADE16058 standard; protein; 1953 AA.
DE G-coupled protein receptor related polypeptide, SEQ ID No 88.
PN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.0%; Score 288.5; DB 7; Length 1953;
Best Local Similarity 31.1%; Pred. No. 4.2e-15;
RESULT 701
ID ADL93997 standard; protein; 1953 AA.
DE Human G-coupled protein receptor-related protein #44.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRHUSEN B D.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAK K.
PA (PATF/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Query Match 16.0%; Score 288.5; DB 8; Length 1953;
Best Local Similarity 31.1%; Pred. No. 4.2e-15;
RESULT 702
ID ADJ83136 standard; protein; 3645 AA.
DE Human hemocentrin protein - SEQ ID 127.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRHUSEN B D.
PA (PATF/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOGF F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 16.0%; Score 288.5; DB 7; Length 3645;
Best Local Similarity 31.1%; Pred. No. 9.8e-15;
RESULT 703
ID ADY74314 standard; protein; 4126 AA.
DE Human hemocentrin protein lacking part of the N-terminus.
PN US6867291-B1.
PD 15-MAR-2005.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 16.0%; Score 288.5; DB 9; Length 4126;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
RESULT 704
ID AEB34668 standard; protein; 4126 AA.
DE Human hemocentrin protein, SEQ ID 4.
PN US2005164277-A1.
PD 28-JUL-2005.
PA (TURN/) TURNER C A.
PA (MATH/) MATHUR B.
PA (DONO/) DONOHO G.
Query Match 16.0%; Score 288.5; DB 9; Length 4126;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
RESULT 705
ID ADY74312 standard; protein; 5518 AA.
DE Human hemocentrin protein.
PN US6867291-B1.
PD 15-MAR-2005.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 16.0%; Score 288.5; DB 9; Length 5518;
Best Local Similarity 31.1%; Pred. No. 1.7e-14;
RESULT 706
ID AEB34666 standard; protein; 5518 AA.
DE Human hemocentrin protein, SEQ ID 2.
PN US2005164277-A1.
PD 28-JUL-2005.
PA (TURN/) TURNER C A.
PA (MATH/) MATHUR B.
PA (DONO/) DONOHO G.
Query Match 16.0%; Score 288.5; DB 9; Length 5518;
Best Local Similarity 31.1%; Pred. No. 1.7e-14;
RESULT 707
ID AEB94406 standard; protein; 5622 AA.
DE Human hemocentrin/FIBL-6 protein, SEQ ID NO: 128.
PN US2005176662-A1.
PD 11-AUG-2005.
PA (UYMI-) UNIV MIAMI.
Query Match 16.0%; Score 288.5; DB 9; Length 5622;
Best Local Similarity 31.1%; Pred. No. 1.8e-14;
RESULT 708
ID ABP60991 standard; protein; 5635 AA.
DE Novel human protein. SEQ ID 78.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 16.0%; Score 288.5; DB 5; Length 5635;
Best Local Similarity 31.1%; Pred. No. 1.8e-14;
RESULT 709
ID ADG39841 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #2.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.

PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 15.9%; Score 287.5; DB 7; Length 1708;
Best Local Similarity 31.1%; Pred. No. 4.3e-15;
RESULT 710
ID ADS98072 standard; protein; 1353 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 336.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 15.8%; Score 285; DB 8; Length 1353;
Best Local Similarity 28.8%; Pred. No. 5.1e-15;
RESULT 711
ID ABB63044 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15924.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 15.8%; Score 284.5; DB 4; Length 467;
Best Local Similarity 26.1%; Pred. No. 1.3e-15;
RESULT 712
ID ADE63330 standard; protein; 858 AA.
DE Rat Protein P13596, SEQ ID NO 9268.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.4%; Score 277.5; DB 7; Length 858;
Best Local Similarity 25.5%; Pred. No. 1.2e-14;
RESULT 713
ID ADZ00014 standard; protein; 858 AA.
DE Rat neural cell adhesion molecule (NCAM) protein SEQ ID NO:44.
PN WO2005030804-A2.
PD 07-APR-2005.
PA (ENKA-) ENKAM PHARM AS.
Query Match 15.4%; Score 277.5; DB 9; Length 858;
Best Local Similarity 25.5%; Pred. No. 1.2e-14;
RESULT 714
ID ADA55624 standard; protein; 733 AA.
DE Human protein, SEQ ID 3192.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.3%; Score 276; DB 6; Length 733;
Best Local Similarity 25.7%; Pred. No. 1.3e-14;
RESULT 715
ID ADE63332 standard; protein; 761 AA.
DE Human Protein P13592, SEQ ID NO 9270.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.3%; Score 276; DB 7; Length 761;
Best Local Similarity 25.7%; Pred. No. 1.4e-14;
RESULT 716
ID RAY89565 standard; protein; 848 AA.
DE Human NCAM 140kd isoform precursor amino acid sequence.
PN WO2000018801-A2.
PD 06-APR-2000.
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.;

PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
Query Match 15.3%; Score 276; DB 3; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.6e-14;
RESULT 717
ID AAB17222 standard; protein; 848 AA.
DE Human 140kd NCAM isoform protein.
PN WO200196364-A2.
PD 20-DEC-2001.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA (UNLO) KINGS COLLEGE LONDON.
Query Match 15.3%; Score 276; DB 5; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.6e-14;
RESULT 718
ID ADI24546 standard; protein; 848 AA.
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:96.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 15.3%; Score 276; DB 8; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.6e-14;
RESULT 719
ID ADV70189 standard; protein; 848 AA.
DE Tumor-associated antigenic target polypeptide TAT434.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 15.3%; Score 276; DB 9; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.6e-14;
RESULT 720
ID ADZ26495 standard; protein; 848 AA.
DE Human CD56.
PN WO2005030999-A1.
PD 07-APR-2005.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 15.3%; Score 276; DB 9; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.6e-14;
RESULT 721
ID ADZ00015 standard; protein; 848 AA.
DE Human neural cell adhesion molecule (NCAM) protein SEQ ID NO:45.
PN WO2005030804-A2.
PD 07-APR-2005.
PA (ENKA-) ENKAM PHARM AS.
Query Match 15.3%; Score 276; DB 9; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.6e-14;
RESULT 722
ID ADF28603 standard; protein; 853 AA.
DE Bovine NCAM-140 protein - SED ID 513.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 15.3%; Score 275.5; DB 7; Length 853;
Best Local Similarity 25.5%; Pred. No. 1.8e-14;
RESULT 723
ID ADL36019 standard; protein; 90 AA.
DE Human NOVX-related polypeptide #17.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.

PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADL/) PADIGARU M.
Query Match 15.2%; Score 275; DB 7; Length 90;
Best Local Similarity 61.8%; Pred. No. 9.1e-16;
RESULT 724
ID ADD25619 standard; protein; 848 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #87.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE-CRAFT INC.
Query Match 15.2%; Score 275; DB 7; Length 848;
Best Local Similarity 25.7%; Pred. No. 2e-14;
RESULT 725
ID ADM95933 standard; protein; 848 AA.
DE Human CD56.
PN WO2005011524-A1.
PD 10-FEB-2005.
PA (CARD-) CARDIO INC.
Query Match 15.2%; Score 275; DB 9; Length 848;
Best Local Similarity 25.7%; Pred. No. 2e-14;
RESULT 726
ID ADX15799 standard; protein; 848 AA.
DE Human CD56.
PN WO2005012512-A1.
PD 10-FEB-2005.
PA (NAXA/) NAKAMURA N.
Query Match 15.2%; Score 275; DB 9; Length 848;
Best Local Similarity 25.7%; Pred. No. 2e-14;
RESULT 727
ID AAE37177 standard; protein; 1477 AA.
DE Human LTRCAPS protein #2.
PN WO2003035831-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 15.2%; Score 274; DB 6; Length 1477;
Best Local Similarity 29.2%; Pred. No. 5.1e-14;
RESULT 728
ID ADH48824 standard; protein; 1356 AA.
DE NOV45B protein sequence, SEQ ID 108.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 273.5; DB 5; Length 1356;
Best Local Similarity 29.8%; Pred. No. 5e-14;
RESULT 729
ID ADH48822 standard; protein; 1426 AA.
DE NOV45A protein sequence, SEQ ID 106.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.0%; Score 271.5; DB 5; Length 1426;
Best Local Similarity 29.6%; Pred. No. 8e-14;
RESULT 730
ID ADZ26717 standard; protein; 858 AA.
DE Human CD56.
PN WO2005030999-A1.
PD 07-APR-2005.
PA (DAND) DANA FARBEN CANCER INST INC.
Query Match 15.0%; Score 271; DB 9; Length 858;
Best Local Similarity 24.8%; Pred. No. 4.4e-14;
RESULT 731
ID AAO30845 standard; protein; 859 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-35.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.0%; Score 271; DB 7; Length 859;
Best Local Similarity 24.8%; Pred. No. 4.4e-14;
RESULT 732
ID ABB68566 standard; protein; 729 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32490.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 15.0%; Score 270; DB 4; Length 729;
Best Local Similarity 26.7%; Pred. No. 4.3e-14;
RESULT 733
ID AAUI8023 standard; protein; 152 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 168.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.9%; Score 269; DB 4; Length 152;
Best Local Similarity 42.3%; Pred. No. 6.1e-15;
RESULT 734
ID ADB31647 standard; protein; 152 AA.
DE Human novel protein SEQ ID NO 168.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.9%; Score 269; DB 7; Length 152;
Best Local Similarity 42.3%; Pred. No. 6.1e-15;
RESULT 735
ID ADR66889 standard; protein; 1469 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 187 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1469;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 736
ID ADR65991 standard; protein; 1469 AA.
DE Human prostatic carcinoma derived protein SEQ ID 187 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1469;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 737
ID ADL35717 standard; protein; 1479 AA.
DE Human peroxidase-melanoma antigen-related protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 14.9%; Score 268.5; DB 8; Length 1479;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 738
ID AAW81030 standard; protein; 1496 AA.
DE Melanoma associated antigen MG50.
PN WO9855133-A1.
PD 10-DEC-1998.
PA (REGC-) UNIV CALIFORNIA.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
Query Match 14.9%; Score 268.5; DB 2; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 739
ID AAY70469 standard; protein; 1496 AA.
DE Human p53 target molecule, PRG2 protein.
PN WO200012526-A1.
PD 09-MAR-2000.
PA (UYPR-) UNIV PRINCETON.
Query Match 14.9%; Score 268.5; DB 3; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 740
ID ABU03498 standard; protein; 1496 AA.
DE Angiogenesis-associated human protein sequence #43.
PN WO200279492-A2.

PD 10-OCT-2002.
PA (ROSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.9%; Score 268.5; DB 6; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 741
ID ADD89024 standard; protein; 1496 AA.
DE TAT264.
PN WO2003057160-A2.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 14.9%; Score 268.5; DB 7; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 742
ID ADF28706 standard; protein; 1496 AA.
DE Human peroxidase-like MG50 protein - SED ID 616.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 7; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 743
ID ADO18902 standard; protein; 1496 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1721.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 744
ID ADQ89920 standard; protein; 1496 AA.
DE Antagonist of cell cycle progression polypeptide #175.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 745
ID ADQ89914 standard; protein; 1496 AA.
DE Antagonist of cell cycle progression polypeptide #172.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 746
ID ADR66092 standard; protein; 1496 AA.
DE Human prostatic carcinoma derived protein SEQ ID 288 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 747
ID ADR66434 standard; protein; 1496 AA.
DE Human prostatic carcinoma derived protein SEQ ID 288 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 748
ID ABB11587 standard; peptide; 1498 AA.
DE Human peroxidase homologue, SEQ ID NO:1957.
PN WO2001571188-A2.
PD 09-AUG-2001.

PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 4; Length 1498;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 749
ID ABO00762 standard; protein; 1498 AA.
DE Polypeptide encoded by novel human contig #13.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 6; Length 1498;
Best Local Similarity 28.8%; Pred. No. 1.5e-13;
RESULT 750
ID AAG02771 standard; protein; 58 AA.
DE Human secreted protein, SEQ ID NO: 6852.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 14.8%; Score 267; DB 3; Length 58;
Best Local Similarity 86.2%; Pred. No. 2.4e-15;
RESULT 751
ID ADV97835 standard; protein; 36946 AA.
DE Murine protein kinase enzyme Seq 155.
PN WO200500200-A2.
PD 06-JAN-2005.
PA (SUGE-) SUGEN INC.
Query Match 14.7%; Score 266; DB 9; Length 36946;
Best Local Similarity 27.6%; Pred. No. 2e-11;
RESULT 752
ID ABB97902 standard; protein; 142 AA.
DE Human secretory polypeptide (SPTM) 154.
PN WO2002020756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 263; DB 5; Length 142;
Best Local Similarity 44.1%; Pred. No. 1.8e-14;
RESULT 753
ID AAY13563 standard; protein; 1395 AA.
DE Drosophila Robo 1 polypeptide.
PN WO9925833-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. No. 6.2e-13;
RESULT 754
ID AAY08401 standard; protein; 1395 AA.
DE Drosophila sp. ROBO1 protein.
PN WO9920764-A1.
PD 29-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. No. 6.2e-13;
RESULT 755
ID ADB85335 standard; protein; 1395 AA.
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.
PN US2003170727-A1.
PD 11-SEP-2003.
PA (GOOD/) GOODMAN C S.
PA (KIDD/) KIDD T.
PA (BROS/) BROSE K.
PA (TESS/) TESSIER-LAVIGNE M.
Query Match 14.5%; Score 261; DB 7; Length 1395;
Best Local Similarity 26.1%; Pred. No. 6.2e-13;
RESULT 756
ID ABB62052 standard; protein; 496 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260.5; DB 4; Length 496;
Best Local Similarity 26.2%; Pred. No. 1.7e-13;
RESULT 757
ID ABB68257 standard; protein; 1395 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260; DB 4; Length 1395;
Best Local Similarity 26.1%; Pred. No. 7.6e-13;
RESULT 758
ID AAY53666 standard; protein; 4412 AA.
DE Sequence g1/1017427/emb/CAA62189 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 14.3%; Score 259; DB 3; Length 4412;
Best Local Similarity 29.6%; Pred. No. 4.5e-12;
RESULT 759
ID ABG74786 standard; protein; 31267 AA.
DE Human RGS11 protein.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 14.3%; Score 259; DB 6; Length 31267;
Best Local Similarity 29.6%; Pred. No. 6.5e-11;
RESULT 760
ID ADQ89964 standard; protein; 34350 AA.
DE Antagonist of cell cycle progression polypeptide #197.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.3%; Score 259; DB 8; Length 34350;
Best Local Similarity 29.6%; Pred. No. 7.4e-11;
RESULT 761
ID ADM74171 standard; protein; 381 AA.
DE Human NOV3A protein sequence SeqID10.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.3%; Score 258.5; DB 8; Length 381;
Best Local Similarity 27.4%; Pred. No. 1.7e-13;
RESULT 762
ID ADM56387 standard; protein; 404 AA.
DE Human cell adhesion molecule NOV12.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.2%; Score 256.5; DB 7; Length 404;
Best Local Similarity 27.4%; Pred. No. 2.8e-13;
RESULT 763
ID ADX44506 standard; protein; 421 AA.
DE Human beta-secretase protein fragment, seqid:1.
PN US6852482-B1.
PD 08-FEB-2005.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 9; Length 421;
Best Local Similarity 26.7%; Pred. No. 3.3e-13;
RESULT 764
ID AAY33741 standard; protein; 444 AA.
DE Beta-secretase.
PN US5942400-A.
PD 24-AUG-1999.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 2; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.5e-13;
RESULT 765
ID AAB47251 standard; protein; 444 AA.
DE Beta-secretase.
PN US6221645-B1.
PD 24-APR-2001.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 4; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.5e-13;
RESULT 766
ID ADX44510 standard; protein; 444 AA.
DE Human beta-secretase protein, seqid:5.
PN US6852482-B1.

PD 08-FEB-2005.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 9; Length 444;
Best Local Similarity 26.7%; Pred. No. 3.5e-13;
RESULT 767
ID ABB63920 standard; protein; 359 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18552.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.1%; Score 255; DB 4; Length 359;
Best Local Similarity 24.9%; Pred. No. 3.2e-13;
RESULT 768
ID ADN4208 standard; protein; 5175 AA.
DE Bacterial polypeptide #6861.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5175;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 769
ID ADN4206 standard; protein; 5175 AA.
DE Bacterial polypeptide #6859.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5175;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 770
ID ADN4207 standard; protein; 5198 AA.
DE Bacterial polypeptide #6860.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 771
ID ADN4205 standard; protein; 5198 AA.
DE Bacterial polypeptide #6858.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.4e-11;
RESULT 772
ID ADM74177 standard; protein; 306 AA.
DE Human NOV3D protein sequence SeqID16.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 306;
Best Local Similarity 27.1%; Pred. No. 3.5e-13;
RESULT 773
ID ABG66677 standard; protein; 404 AA.
DE Human novel polypeptide #12.
PN WO200244340-A2.
PD 06-JUN-2002.

```
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253.5; DB 5; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.1e-13;
RESULT 774
ID ABB760221 standard; protein; 404 AA.
DE Human IG gene related protein SEQ ID NO 44.
PN WO20029040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 14.0%; Score 253.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.1e-13;
RESULT 775
ID ADF66751 standard; protein; 404 AA.
DE Novel human protein NOV12.
PN US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.1e-13;
RESULT 776
ID ADI19788 standard; protein; 404 AA.
DE Human NOV12 protein.
PN US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.1e-13;
RESULT 777
ID ADO60261 standard; protein; 404 AA.
DE Human NOV12 protein.
PN US2003134430-A1.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 5.1e-13;
RESULT 778
ID ADO47378 standard; protein; 568 AA.
DE Human neurotrophin-like protein-related protein SeqID13.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 14.0%; Score 253; DB 8; Length 568;
Best Local Similarity 27.4%; Pred. No. 8.9e-13;
RESULT 779
ID ABB76023 standard; protein; 570 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253; DB 4; Length 570;
Best Local Similarity 27.4%; Pred. No. 9e-13;
RESULT 780
ID ABB76018 standard; protein; 586 AA.
DE Neurotrophin-like polypeptide splice variant.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.0%; Score 253; DB 4; Length 586;
Best Local Similarity 27.4%; Pred. No. 9.3e-13;
RESULT 781
ID ADO47372 standard; protein; 586 AA.
DE Human neurotrophin-like protein SeqID7.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 14.0%; Score 253; DB 8; Length 586;
Best Local Similarity 27.4%; Pred. No. 9.3e-13;
RESULT 782
ID ABO23244 standard; protein; 404 AA.
DE Human breast tumour associated protein 47-like polypeptide NOV12.
PN US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.9%; Score 251.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 7.6e-13;
RESULT 783
ID AAB61142 standard; protein; 404 AA.
DE Human NOV12 protein.
PN WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match 13.9%; Score 250.5; DB 4; Length 404;
Best Local Similarity 27.1%; Pred. No. 9.2e-13;
RESULT 784
ID ABB61502 standard; protein; 885 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11298.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.9%; Score 250.5; DB 4; Length 885;
Best Local Similarity 26.5%; Pred. No. 2.7e-12;
RESULT 785
ID ABB76016 standard; protein; 374 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 374;
Best Local Similarity 27.7%; Pred. No. 9.2e-13;
RESULT 786
ID ADO47381 standard; protein; 374 AA.
DE Human neurotrophin-like protein-related protein SeqID16.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 374;
Best Local Similarity 27.7%; Pred. No. 9.2e-13;
RESULT 787
ID ADO47377 standard; protein; 440 AA.
DE Human neurotrophin-like protein-related protein SeqID12.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 440;
Best Local Similarity 27.7%; Pred. No. 1.1e-12;
RESULT 788
ID ABB76022 standard; protein; 442 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 442;
Best Local Similarity 27.7%; Pred. No. 1.2e-12;
RESULT 789
ID ABB76017 standard; protein; 458 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 458;
Best Local Similarity 27.7%; Pred. No. 1.2e-12;
RESULT 790
ID ADO47369 standard; protein; 458 AA.
DE Human neurotrophin-like protein SeqID4.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 458;
Best Local Similarity 27.7%; Pred. No. 1.2e-12;
RESULT 791
ID ADS10607 standard; protein; 458 AA.
DE Human therapeutic protein - SEQ ID 844.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.8%; Score 250; DB 8; Length 458;
```

Best Local Similarity 27.7%; Pred. No. 1.2e-12;
RESULT 792
ID ADO47385 standard; protein; 880 AA.
DE Human neurotrophin-like protein-related protein SeqID13.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 880;
Best Local Similarity 27.7%; Pred. No. 3e-12;
RESULT 793
ID AAO30844 standard; protein; 886 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-34.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.8%; Score 250; DB 7; Length 886;
Best Local Similarity 27.7%; Pred. No. 3e-12;
RESULT 794
ID ADO47396 standard; protein; 955 AA.
DE Human neurotrophin-like protein-related MAM domain GPIM protein SeqID31.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 3.3e-12;
RESULT 795
ID ADO47383 standard; protein; 955 AA.
DE Human neurotrophin-like protein SeqID18.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match 13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 3.3e-12;
RESULT 796
ID ADS10608 standard; protein; 955 AA.
DE Human therapeutic protein - SEQ ID 845.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.8%; Score 250; DB 8; Length 955;
Best Local Similarity 27.7%; Pred. No. 3.3e-12;
RESULT 797
ID ADS11107 standard; protein; 970 AA.
DE Human therapeutic protein - SEQ ID 1344.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 13.8%; Score 250; DB 8; Length 970;
Best Local Similarity 27.7%; Pred. No. 3.4e-12;
RESULT 798
ID ABG12100 standard; protein; 1219 AA.
DE Novel human diagnostic protein #12091.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 250; DB 4; Length 1219;
Best Local Similarity 27.7%; Pred. No. 4.6e-12;
RESULT 799
ID ABUS2336 standard; protein; 1315 AA.
DE Human GPCR related protein NOV13a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 6; Length 1315;
Best Local Similarity 27.7%; Pred. No. 5.1e-12;
RESULT 800
ID ADH72138 standard; protein; 1315 AA.
DE Human protein of the invention NOV46h SEQ ID NO:1034.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 8; Length 1315;
Best Local Similarity 27.7%; Pred. No. 5.1e-12;

RESULT 801
ID ADL24007 standard; protein; 1315 AA.
DE Human NOVX polypeptide #26.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUF/) TAUFIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENNA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 13.8%; Score 250; DB 8; Length 1315;
Best Local Similarity 27.7%; Pred. No. 5.1e-12;
RESULT 802
ID ADH72134 standard; protein; 1335 AA.
DE Human protein of the invention NOV46f SEQ ID NO:1030.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 8; Length 1335;
Best Local Similarity 27.7%; Pred. No. 5.2e-12;
RESULT 803
ID ABUS2329 standard; protein; 1386 AA.
DE Human GPCR related protein NOV12a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 6; Length 1386;
Best Local Similarity 27.7%; Pred. No. 5.5e-12;
RESULT 804
ID ADL23993 standard; protein; 1386 AA.
DE Human NOVX polypeptide #19.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.

PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENNA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHINKETS R A.
PA (RAST/) RASTELLI L S.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match
Best Local Similarity 13.8%; Score 250; DB 8; Length 1386;
Best Local Similarity 27.7%; Pred. No. 5.5e-12;
RESULT 805
ID ADD47172 standard; protein; 1040 AA.
DE Human protein NP_005067, SEQ ID NO 12866.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO/) GEN HOSPITAL CORP.
PA (FARB/) BAYER AG.
Query Match
Best Local Similarity 13.8%; Score 249.5; DB 7; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.1e-12;
RESULT 806
ID ADO28581 standard; protein; 1040 AA.
DE Human axonin-1 precursor (AXO1) protein SEQ ID NO:10.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.1e-12;
RESULT 807
ID ABO84729 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.1e-12;
RESULT 808
ID ABO84728 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 4.1e-12;
RESULT 809
ID ABB68882 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33438.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match
Best Local Similarity 13.7%; Score 248; DB 4; Length 467;
Best Local Similarity 27.4%; Pred. No. 1.8e-12;
RESULT 810
ID ADJ68312 standard; protein; 1007 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID118.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 13.6%; Score 246.5; DB 7; Length 1007;
Best Local Similarity 24.6%; Pred. No. 7.1e-12;

RESULT 811
ID AAR63759 standard; protein; 1018 AA.
DE Human contactin (EMBL Accession #Z21488).
PN EP618293-A1.
PD 05-OCT-1994.
PA (BECT/) BECTON DICKINSON CO.
Query Match
Best Local Similarity 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.2e-12;
RESULT 812
ID AAR87028 standard; protein; 1018 AA.
DE Human contactin.
PN WO9535373-A2.
PD 28-DEC-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match
Best Local Similarity 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.2e-12;
RESULT 813
ID ADE71113 standard; protein; 1018 AA.
DE Contactin, SEQ ID 67.
PN WO2003070889-A2.
PD 28-AUG-2003.
PA (IDEC-) IDEC PHARM CORP.
Query Match
Best Local Similarity 13.6%; Score 246.5; DB 7; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.2e-12;
RESULT 814
ID ADJ75696 standard; protein; 1018 AA.
DE Marker gene related amino acid sequence SEQ ID NO:948.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.2e-12;
RESULT 815
ID ADO28659 standard; protein; 1018 AA.
DE Human CONT protein SEQ ID NO:88.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.2e-12;
RESULT 816
ID ADP67246 standard; protein; 1018 AA.
DE Human F3/Contactin protein.
PN WO2004052389-A2.
PD 24-JUN-2004.
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
Query Match
Best Local Similarity 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.2e-12;
RESULT 817
ID ADR66068 standard; protein; 1073 AA.
DE Human prostatic carcinoma derived protein SEQ ID 264 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 13.6%; Score 245.5; DB 8; Length 1073;
Best Local Similarity 26.4%; Pred. No. 9.5e-12;
RESULT 818
ID ADR66410 standard; protein; 1073 AA.
DE Human prostatic carcinoma derived protein SEQ ID 264 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 13.6%; Score 245.5; DB 8; Length 1073;
Best Local Similarity 26.4%; Pred. No. 9.5e-12;

```
RESULT 819
ID ADA54925 standard; protein; 512 AA.
DE Human protein, SEQ ID 2493.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.5%; Score 244.5; DB 6; Length 512;
Best Local Similarity 27.8%; Pred. No. 4.2e-12;
RESULT 820
ID AAW06485 standard; peptide; 1018 AA.
DE Rat contactin ligand for RPRbeta.
PN WO9637776-A1.
PD 28-NOV-1996.
PA (SUGE-) SUGEN INC.
Query Match 13.5%; Score 243.5; DB 2; Length 1018;
Best Local Similarity 24.0%; Pred. No. 1.3e-11;
RESULT 821
ID ADE56173 standard; protein; 1021 AA.
DE Rat Protein Q63198, SEQ ID NO 2022.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.5%; Score 243.5; DB 7; Length 1021;
Best Local Similarity 24.0%; Pred. No. 1.3e-11;
RESULT 822
ID ABG03059 standard; protein; 792 AA.
DE Novel human diagnostic protein #3050.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 792;
Best Local Similarity 26.4%; Pred. No. 1.1e-11;
RESULT 823
ID ABG00258 standard; protein; 893 AA.
DE Novel human diagnostic protein #249.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 893;
Best Local Similarity 26.4%; Pred. No. 1.3e-11;
RESULT 824
ID ABG00611 standard; protein; 893 AA.
DE Novel human diagnostic protein #602.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 242.5; DB 4; Length 893;
Best Local Similarity 26.4%; Pred. No. 1.3e-11;
RESULT 825
ID ABG31317 standard; protein; 2586 AA.
DE Human 5+3 corrected OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 5; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 826
ID ABG32891 standard; protein; 2586 AA.
DE Human osteoclast protein (OCP) #1.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
ID ADL02231 standard; protein; 2586 AA.
DE Human OCP protein #1.
PN WO9604396-A1.
DE Human OCP protein #1.
```

```
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 828
ID ADL02234 standard; protein; 2586 AA.
DE Human OCP protein #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2586;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 829
ID AAB47935 standard; protein; 2587 AA.
DE Human OCP.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2587;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 830
ID ABG32896 standard; protein; 2587 AA.
DE Human osteoclast protein (OCP) #2.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 13.4%; Score 242; DB 5; Length 2587;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 831
ID ADL02236 standard; protein; 2587 AA.
DE Human OCP protein #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 8; Length 2587;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 832
ID ABG31323 standard; protein; 2589 AA.
DE Human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 5; Length 2589;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 833
ID ADL02244 standard; protein; 2589 AA.
DE Human OCP protein #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.4%; Score 242; DB 5; Length 2589;
Best Local Similarity 27.0%; Pred. No. 6.3e-11;
RESULT 834
ID AAR92256 standard; protein; 582 AA.
DE Neural cell adhesion molecule splice variant.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Query Match 13.4%; Score 241.5; DB 2; Length 582;
Best Local Similarity 24.4%; Pred. No. 9.1e-12;
RESULT 835
ID AAR92255 standard; protein; 761 AA.
DE Neural cell adhesion molecule.
PN WO9604396-A1.
```



```
Query Match      13.0%; Score 235.5; DB 8; Length 2428;
Best Local Similarity 26.9%; Pred. No. 2.1e-10;
RESULT 854
ID ADL02252 standard; protein; 2623 AA.
DE Human OCP protein #7.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match      13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2.3e-10;
RESULT 855
ID ADS10577 standard; protein; 2623 AA.
DE Human therapeutic protein - SEQ ID 814.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match      13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2.3e-10;
RESULT 856
ID ADN24073 standard; protein; 662 AA.
DE Bacterial polypeptide #6726.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      13.0%; Score 235; DB 8; Length 662;
Best Local Similarity 25.5%; Pred. No. 3.9e-11;
RESULT 857
ID ADD47171 standard; protein; 1040 AA.
DE Rat Protein AAA42201, SEQ ID NO 12864.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match      13.0%; Score 234.5; DB 7; Length 1040;
Best Local Similarity 25.8%; Pred. No. 8.1e-11;
RESULT 858
ID ADR67266 standard; protein; 1100 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match      12.9%; Score 233.5; DB 8; Length 1100;
Best Local Similarity 24.9%; Pred. No. 1.1e-10;
RESULT 859
ID ADH71816 standard; protein; 967 AA.
DE Human protein of the invention NOV29x SEQ ID NO:712.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match      12.9%; Score 232.5; DB 8; Length 967;
Best Local Similarity 26.8%; Pred. No. 1.1e-10;
RESULT 860
ID ADN23691 standard; protein; 2783 AA.
DE Bacterial polypeptide #6344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      12.9%; Score 232.5; DB 8; Length 2783;
Best Local Similarity 23.5%; Pred. No. 4.6e-10;
RESULT 861
Query Match      13.0%; Score 235.5; DB 8; Length 2428;
Best Local Similarity 26.9%; Pred. No. 2.1e-10;
RESULT 854
ID ADL02252 standard; protein; 2623 AA.
DE Human OCP protein #7.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match      13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2.3e-10;
RESULT 855
ID ADS10577 standard; protein; 2623 AA.
DE Human therapeutic protein - SEQ ID 814.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match      13.0%; Score 235; DB 8; Length 662;
Best Local Similarity 25.5%; Pred. No. 3.9e-11;
RESULT 857
ID ADD47171 standard; protein; 1040 AA.
DE Rat Protein AAA42201, SEQ ID NO 12864.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match      13.0%; Score 234.5; DB 7; Length 1040;
Best Local Similarity 25.8%; Pred. No. 8.1e-11;
RESULT 858
ID ADR67266 standard; protein; 1100 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match      12.9%; Score 233.5; DB 8; Length 1100;
Best Local Similarity 24.9%; Pred. No. 1.1e-10;
RESULT 859
ID ADH71816 standard; protein; 967 AA.
DE Human protein of the invention NOV29x SEQ ID NO:712.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match      12.9%; Score 232.5; DB 8; Length 967;
Best Local Similarity 26.8%; Pred. No. 1.1e-10;
RESULT 860
ID ADN23691 standard; protein; 2783 AA.
DE Bacterial polypeptide #6344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      12.9%; Score 232.5; DB 8; Length 2783;
Best Local Similarity 23.5%; Pred. No. 4.6e-10;
RESULT 861
Query Match      12.8%; Score 232; DB 5; Length 2401;
Best Local Similarity 26.9%; Pred. No. 4.2e-10;
RESULT 862
ID ABG69619 standard; protein; 2447 AA.
DE Human NOV12f protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match      12.8%; Score 232; DB 5; Length 2447;
Best Local Similarity 26.9%; Pred. No. 4.3e-10;
RESULT 863
ID ADJ83065 standard; protein; 2591 AA.
DE Human NOVX NOV12f protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEFLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match      12.8%; Score 232; DB 7; Length 2591;
Best Local Similarity 26.9%; Pred. No. 4.6e-10;
RESULT 864
ID ADH71822 standard; protein; 2591 AA.
DE Human protein of the invention NOV29aa SEQ ID NO:718.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match      12.8%; Score 232; DB 8; Length 2591;
Best Local Similarity 26.9%; Pred. No. 4.6e-10;
RESULT 865
ID ADH71820 standard; protein; 2602 AA.
DE Human protein of the invention NOV29z SEQ ID NO:716.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match      12.8%; Score 232; DB 8; Length 2602;
Best Local Similarity 26.9%; Pred. No. 4.6e-10;
RESULT 866
ID ADJ83055 standard; protein; 2617 AA.
DE Human NOVX NOV12a protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
```


PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET Y.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 12.8%; Score 232; DB 7; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 867
ID ADH71842 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ak SEQ ID NO:738.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 868
ID ADH71852 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ap SEQ ID NO:748.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 869
ID ADH71838 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ai SEQ ID NO:734.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 870
ID ADH71770 standard; protein; 2617 AA.
DE Human protein of the invention NOV29a SEQ ID NO:666.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 871
ID ADH71836 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ah SEQ ID NO:732.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 872
ID ADH71840 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aj SEQ ID NO:736.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 873
ID ADH71844 standard; protein; 2617 AA.
DE Human protein of the invention NOV29al SEQ ID NO:740.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 874
ID ADH71846 standard; protein; 2617 AA.
DE Human protein of the invention NOV29am SEQ ID NO:742.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 875
ID ADH71850 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ao SEQ ID NO:746.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 876
ID ADH71854 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aq SEQ ID NO:750.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 877
ID ADH71848 standard; protein; 2617 AA.
DE Human protein of the invention NOV29an SEQ ID NO:744.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.7e-10;
RESULT 878
ID ABO07377 standard; protein; 3931 AA.
DE Human protein NOV9.
PN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 232; DB 6; Length 3931;
Best Local Similarity 28.3%; Pred. No. 8.2e-10;
RESULT 879
ID AAW29667 standard; protein; 1028 AA.
DE Homo sapiens DL185_1 clone secreted protein.
PN WO9830655-A2.
PD 16-JUL-1998.
PA (GEMY) GENETICS INST INC.
Query Match 12.8%; Score 231; DB 2; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.6e-10;
RESULT 880
ID ADP67247 standard; protein; 1028 AA.
DE Human NB-3 protein.
PN WO2004052389-A2.
PD 24-JUN-2004.
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FOR/) FORREST G R.
Query Match 12.8%; Score 231; DB 8; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.6e-10;
RESULT 881
ID ADG39786 standard; protein; 3931 AA.
DE Human novel protein NOV9.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.

```
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 12.8%; Score 231; DB 7; Length 3931;
Best Local Similarity 28.3%; Pred. No. 9.9e-10;
RESULT 882
ID AAW26507 standard; protein; 868 AA.
DE Rat Dmk receptor.
PN US5656473-A.
PD 12-AUG-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 883
ID AAW26610 standard; protein; 868 AA.
DE Rat muscle-specific kinase (MusK).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 884
ID ADH71830 standard; protein; 961 AA.
DE Human protein of the invention NOV29ae SEQ ID NO:726.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CUR-) CURAGEN CORP.
Query Match 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.6e-10;
RESULT 885
ID ADH71832 standard; protein; 961 AA.
DE Human protein of the invention NOV29af SEQ ID NO:728.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CUR-) CURAGEN CORP.
Query Match 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.6e-10;
RESULT 886
ID ABO84727 standard; protein; 1040 AA.
DE Mouse cancer-associated protein MP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 230.5; DB 8; Length 1040;
Best Local Similarity 25.0%; Pred. No. 1.8e-10;
RESULT 887
ID ABO84469 standard; protein; 3475 AA.
DE Human cancer-associated protein HPI3-036.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 230.5; DB 8; Length 3475;
Best Local Similarity 24.3%; Pred. No. 9.3e-10;
RESULT 888
ID ADG39842 standard; protein; 1928 AA.
DE Protein similar to human NOV9 #3.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
Query Match 12.7%; Score 230; DB 7; Length 1928;
Best Local Similarity 22.9%; Pred. No. 4.6e-10;
RESULT 889
ID ADG39843 standard; protein; 1951 AA.
DE Protein similar to human NOV9 #4.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 12.7%; Score 230; DB 7; Length 1928;
Best Local Similarity 22.9%; Pred. No. 4.6e-10;
RESULT 890
ID AAY35667 standard; protein; 3117 AA.
DE Sequence gi/3328186 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 12.7%; Score 230; DB 3; Length 3117;
Best Local Similarity 22.9%; Pred. No. 8.8e-10;
RESULT 891
ID AAB31889 standard; protein; 4393 AA.
DE Amino acid sequence of a human protein.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INNR-) BIOMERIEUX STELHYS.
Query Match 12.7%; Score 230; DB 4; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.4e-09;
RESULT 892
ID ADL35758 standard; protein; 4393 AA.
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.4e-09;
RESULT 893
ID ADQ39442 standard; protein; 4393 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1105.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.4e-09;
RESULT 894
ID ABG23265 standard; protein; 4436 AA.
DE Novel human diagnostic protein #23256.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 230; DB 4; Length 4436;
Best Local Similarity 26.0%; Pred. No. 1.4e-09;
RESULT 895
ID ADL16585 standard; protein; 849 AA.
DE Human 282PIG3 polypeptide #35.
```

PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 849;
Best Local Similarity 25.6%; Pred. No. 1.6e-10;
RESULT 896
ID ADL16586 standard; protein; 851 AA.
DE Human 282P1G3 polypeptide #36.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 851;
Best Local Similarity 25.6%; Pred. No. 1.7e-10;
RESULT 897
ID AAW26506 standard; protein; 869 AA.
DE Human Dmk receptor.
PN US5656473-A.
PD 12-AUG-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.7e-10;
RESULT 898
ID AAW26611 standard; protein; 869 AA.
DE Human muscle-specific kinase (MuSK).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.7e-10;
RESULT 899
ID ADQ89844 standard; protein; 869 AA.
DE Antagonist of cell cycle progression polypeptide #137.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 12.7%; Score 229.5; DB 8; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.7e-10;
RESULT 900
ID ADL16446 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #12.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.8e-10;
RESULT 901
ID ADL16584 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #34.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.8e-10;
RESULT 902
ID ADL16625 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #57.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.8e-10;
RESULT 903
ID ADL16431 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #3.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.8e-10;
RESULT 904
ID ADL16626 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #58.
PN WO2004016734-A2.

PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 905
ID ADL16590 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #37.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 906
ID ADL16447 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #13.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 907
ID ADL16433 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #4.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 908
ID ADL16592 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #39.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 909
ID ABM83685 standard; protein; 1171 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3934.
PN WO2004033973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.7%; Score 229.5; DB 8; Length 1171;
Best Local Similarity 25.6%; Pred. No. 2.6e-10;
RESULT 910
ID ADL16604 standard; protein; 1183 AA.
DE Human 282P1G3 polypeptide #45.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.6e-10;
RESULT 911
ID ADL16628 standard; protein; 1183 AA.
DE Human 282P1G3 polypeptide #60.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.6e-10;
RESULT 912
ID ADL16449 standard; protein; 1183 AA.
DE Human 282P1G3 polypeptide #15.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.6e-10;
RESULT 913
ID ADL16602 standard; protein; 1183 AA.
DE Human 282P1G3 polypeptide #43.
PN WO2004016734-A2.
PD 26-FEB-2004.

PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.6e-10;
RESULT 914
ID ADL16437 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #6.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.6e-10;
RESULT 915
ID ADL16448 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #14.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 916
ID ADL16596 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #40.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 917
ID ADL16435 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #5.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 918
ID ADL16627 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #59.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 919
ID ADL16598 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #42.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 920
ID ADJ69602 standard; protein; 1224 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1408.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.7%; Score 229.5; DB 7; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 921
ID ADL16443 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #9.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 922
ID ADL16597 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #41.
PN WO2004016734-A2.
PD 26-FEB-2004.

PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 923
ID ADL16621 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #53.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 924
ID ADL16452 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #18.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 925
ID ADL16623 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #55.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 926
ID ADL16579 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #32.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 927
ID ADL16427 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #1.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 928
ID ADL16455 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #21.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 929
ID ADL16457 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #23.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 930
ID ADL16591 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #38.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.7e-10;
RESULT 931
ID ADL16620 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #52.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.

```
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 932
ID ADL16456 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #22.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 933
ID ADL16615 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #50.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 934
ID ADL16622 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #54.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 935
ID ADL16444 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #10.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 936
ID ADL16458 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #24.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 937
ID ADL16550 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #27.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 938
ID ADL16459 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #25.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 939
ID ADL16603 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #44.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 940
ID ADL16453 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #19.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 941
ID ADL16632 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #63.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 942
ID ADL16609 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #47.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match      12.7%  Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%  Pred. No. 2.7e-10;
RESULT 943
ID ADQ39441 standard; protein; 3588 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1104.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match      12.7%  Score 229; DB 8; Length 3588;
Best Local Similarity 26.0%  Pred. No. 1.3e-09;
RESULT 944
ID ADQ39440 standard; protein; 4346 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1103.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match      12.7%  Score 229; DB 8; Length 4346;
Best Local Similarity 26.0%  Pred. No. 1.7e-09;
RESULT 945
ID ADQ39439 standard; protein; 4347 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1102.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match      12.7%  Score 229; DB 8; Length 4347;
Best Local Similarity 26.0%  Pred. No. 1.7e-09;
RESULT 946
ID ADJ69461 standard; protein; 4370 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1267.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match      12.7%  Score 229; DB 7; Length 4370;
Best Local Similarity 26.0%  Pred. No. 1.7e-09;
RESULT 947
ID ABG16336 standard; protein; 1493 AA.
DE Novel human diagnostic protein #16327.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match      12.6%  Score 228; DB 4; Length 1493;
Best Local Similarity 24.1%  Pred. No. 4.8e-10;
RESULT 948
ID ADV97842 standard; protein; 8523 AA.
DE Murine protein kinase enzyme Seq 162.
PN WO200500200-A2.
PD 06-JAN-2005.
PA (SUGE-) SUGEN INC.
Query Match      12.6%  Score 227.5; DB 9; Length 8523;
Best Local Similarity 25.6%  Pred. No. 5.7e-09;
RESULT 949
ID ADN22360 standard; protein; 6642 AA.
DE Bacterial polypeptide #5013.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
```

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 226; DB 8; Length 6642;
Best Local Similarity 23.7%; Pred. No. 5.5e-09;
RESULT 950
ID AAR92718 standard; protein; 478 AA.
DE Mouse muscle-localized protein-tyrosine-kinase receptor 5' fragment.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 478;
Best Local Similarity 24.8%; Pred. No. 1.7e-10;
RESULT 951
ID AAR92716 standard; protein; 860 AA.
DE Mouse muscle-localised protein-tyrosine-kinase receptor-1 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 860;
Best Local Similarity 24.8%; Pred. No. 3.7e-10;
RESULT 952
ID AAR92717 standard; protein; 868 AA.
DE Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMY) GENETICS INST INC.
Query Match 12.5%; Score 225.5; DB 2; Length 868;
Best Local Similarity 24.8%; Pred. No. 3.8e-10;
RESULT 953
ID ABJ10922 standard; protein; 869 AA.
DE Human secreted protein (SECP) #18.
PN WO200270669-A2.
PD 12-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.5%; Score 225.5; DB 5; Length 869;
Best Local Similarity 29.5%; Pred. No. 3.8e-10;
RESULT 954
ID AAE34390 standard; protein; 4391 AA.
DE Human perlecan protein.
PN WO200295415-A2.
PD 28-NOV-2002.
PA (OSTE-) OSTEOMETER BIO TECH AS.
Query Match 12.5%; Score 225; DB 6; Length 4391;
Best Local Similarity 25.7%; Pred. No. 3.8e-09;
RESULT 955
ID ADW16038 standard; protein; 477 AA.
DE Human FGFR5 splice variant #4, SEQ ID 23.
PN US2005009750-A1.
PD 13-JAN-2005.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 12.4%; Score 224.5; DB 9; Length 477;
Best Local Similarity 22.7%; Pred. No. 2e-10;
RESULT 956
ID AEA05858 standard; protein; 477 AA.
DE Human fibroblast growth factor receptor 5 splice variant, SEQ.23.
PN US2005112642-A1.
PD 26-MAY-2005.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 12.4%; Score 224.5; DB 9; Length 477;
Best Local Similarity 22.7%; Pred. No. 2e-10;
RESULT 957
ID ABG74129 standard; protein; 537 AA.
DE Human hMusk-R deletion mutant mMusk-RI.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match 12.4%; Score 224.5; DB 4; Length 537;
Best Local Similarity 26.0%; Pred. No. 2.4e-10;
ID AAG77857 standard; protein; 537 AA.
DE Mutant protein mMusk-RI.

PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 537;
Best Local Similarity 26.0%; Pred. No. 2.4e-10;
RESULT 959
ID ABG74130 standard; protein; 576 AA.
DE Human hMusk-R deletion mutant mMusk-RII.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match 12.4%; Score 224.5; DB 4; Length 576;
Best Local Similarity 26.0%; Pred. No. 2.6e-10;
RESULT 960
ID AAG77858 standard; protein; 576 AA.
DE Mutant protein mMusk-RII.
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 576;
Best Local Similarity 26.0%; Pred. No. 2.6e-10;
RESULT 961
ID ABG74128 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor, hMusk-R.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match 12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4.6e-10;
RESULT 962
ID AAB68421 standard; protein; 869 AA.
DE Amino acid sequence of a human Musk-R polypeptide.
PN WO200136659-A2.
PD 25-MAY-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4.6e-10;
RESULT 963
ID AAG77856 standard; protein; 869 AA.
DE Protein of muscle specific tyrosine kinase receptor (hMusk-R).
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4.6e-10;
RESULT 964
ID ADS17276 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor (Musk-R) protein fragment.
PN US6790614-B1.
PD 14-SEP-2004.
PA (NOVS) NOVARTIS AG.
Query Match 12.4%; Score 224.5; DB 8; Length 869;
Best Local Similarity 26.0%; Pred. No. 4.6e-10;
RESULT 965
ID ABG22633 standard; protein; 981 AA.
DE Novel human diagnostic protein #22624.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 981;
Best Local Similarity 23.9%; Pred. No. 5.4e-10;
RESULT 966
ID ADR08740 standard; protein; 1113 AA.
DE Human protein useful for treating neurological disease Seq 2246.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 12.4%; Score 224.5; DB 8; Length 1113;
Best Local Similarity 25.3%; Pred. No. 6.4e-10;
RESULT 967
ID ADL16578 standard; protein; 1171 AA.
DE Human 282P1G3 polypeptide #31.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6.9e-10;
RESULT 968
ID ADL16624 standard; protein; 1171 AA.
DE Human 282P1G3 polypeptide #56.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6.9e-10;
RESULT 969
ID ADL16580 standard; protein; 1171 AA.
DE Human 282P1G3 polypeptide #33.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6.9e-10;
RESULT 970
ID ADL16429 standard; protein; 1171 AA.
DE Human 282P1G3 polypeptide #2.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6.9e-10;
RESULT 971
ID ADL16445 standard; protein; 1171 AA.
DE Human 282P1G3 polypeptide #11.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1171;
Best Local Similarity 25.3%; Pred. No. 6.9e-10;
RESULT 972
ID ADE55236 standard; protein; 1224 AA.
DE Human Protein AAB60937, SEQ ID NO 1049.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.4%; Score 224.5; DB 7; Length 1224;
Best Local Similarity 25.3%; Pred. No. 7.3e-10;
RESULT 973
ID ADL15032 standard; protein; 1224 AA.
DE Human neural cell adhesion molecule protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 12.4%; Score 224.5; DB 7; Length 1224;
Best Local Similarity 25.3%; Pred. No. 7.3e-10;
RESULT 974
ID ADJ75519 standard; protein; 1224 AA.
DE Marker gene related amino acid sequence SEQ ID NO:771.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 7.3e-10;
RESULT 975
ID ADL16454 standard; protein; 1224 AA.
DE Human 282P1G3 polypeptide #20.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.

Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 7.3e-10;
RESULT 976
ID ADN04062 standard; protein; 1224 AA.
DE Antipsoriatic protein sequence #226.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 7.3e-10;
RESULT 977
ID ADQ19766 standard; protein; 1224 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2585.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 7.3e-10;
RESULT 978
ID ADR14776 standard; protein; 1224 AA.
DE Amino acid sequence of human MAPKAX orthologue #8.
PN WO2004086948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1224;
Best Local Similarity 25.3%; Pred. No. 7.3e-10;
RESULT 979
ID ADP29420 standard; protein; 1583 AA.
DE Human secreted protein SEQ ID #187.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1583;
Best Local Similarity 23.9%; Pred. No. 1e-09;
RESULT 980
ID ADP29354 standard; protein; 1583 AA.
DE Human secreted protein SEQ ID #121.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.4%; Score 224.5; DB 8; Length 1583;
Best Local Similarity 23.9%; Pred. No. 1e-09;
RESULT 981
ID ABG20008 standard; protein; 1645 AA.
DE Novel human diagnostic protein #19999.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 1645;
Best Local Similarity 23.9%; Pred. No. 1.1e-09;
RESULT 982
ID ABG22631 standard; protein; 1765 AA.
DE Novel human diagnostic protein #22622.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 1765;
Best Local Similarity 23.9%; Pred. No. 1.2e-09;
RESULT 983
ID ABG12017 standard; protein; 1944 AA.
DE Novel human diagnostic protein #12008.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224.5; DB 4; Length 1944;
Best Local Similarity 23.9%; Pred. No. 1.4e-09;
RESULT 984
ID AAE30259 standard; peptide; 68 AA.
DE Human LP289 protein immunoglobulin-like domain #1.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (LIL) LILLY & CO ELI.
Query Match 12.4%; Score 224; DB 6; Length 68;

```
Best Local Similarity 65.7%; Pred. No. 1.6e-11;
RESULT 985
ID ABG02117 standard; protein; 434 AA.
DE Novel human diagnostic protein #2108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224; DB 4; Length 434;
Best Local Similarity 25.5%; Pred. No. 2e-10;
RESULT 986
ID AAM93829 standard; protein; 697 AA.
DE Human polypeptide, SEQ ID NO: 3893.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.4%; Score 224; DB 4; Length 697;
Best Local Similarity 23.9%; Pred. No. 3.8e-10;
RESULT 987
ID ADL31860 standard; protein; 697 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3893.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.4%; Score 224; DB 8; Length 697;
Best Local Similarity 23.9%; Pred. No. 3.8e-10;
RESULT 988
ID ABG02019 standard; protein; 737 AA.
DE Novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224; DB 4; Length 737;
Best Local Similarity 25.5%; Pred. No. 4e-10;
RESULT 989
ID AAY08095 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 990
ID AAY13393 standard; protein; 1059 AA.
DE Amino acid sequence of protein PRO335.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 991
ID AAY70672 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 992
ID ADC78602 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 993
ID AAB80261 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 994
ID AAU00825 standard; protein; 1059 AA.
DE Human immune response protein PRO335 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 995
ID ABU71639 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 996
ID ABU71494 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 997
ID ABU71940 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 998
ID ABO01823 standard; protein; 1059 AA.
DE Novel human secreted and transmembrane protein PRO335.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 999
ID ABU54396 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1000
ID ABO47411 standard; protein; 1059 AA.
DE Human secreted/transmembrane polypeptide PRO335.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1001
ID ABU64548 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #52.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1002
ID ABU67394 standard; protein; 1059 AA.
DE Human secreted protein PRO335.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1003
```


PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1022
ID ADC39798 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1023
ID ADC40312 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1024
ID ADC19136 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1025
ID ADC34436 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1026
ID ADC29491 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049676-A1;
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1027
ID ADC29022 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1028
ID ADC40907 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1029
ID ADC19564 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1030
ID ADC34012 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003073077-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1031
ID ADC13082 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1032
ID ADC12534 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1033
ID ADD05089 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1034
ID ADD04095 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1035
ID ADD03671 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1036
ID ADE34923 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1037
ID ADH59406 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1038
ID ADI38185 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1039
ID ADJ26453 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054349-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1040
ID ADE79368 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1041
ID ADE79792 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1042
ID ADE73468 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1043
ID ADE74003 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1044
ID ADE99557 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1045
ID ADE98676 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1046
ID ADE99103 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1047
ID ADC40573 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1048
ID ADF73967 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1049
ID ADF73543 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1050
ID ADG92386 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1051
ID ADG92813 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1052
ID ADH20602 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1053
ID ADH07457 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1054
ID ADH60002 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211590-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1055
ID ADH07030 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.

```
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1056
ID ADI18772 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003152939-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1057
ID ADI65492 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003148419-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1058
ID ADI37751 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003096340-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1059
ID ADH97551 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003190610-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1060
ID ADI65919 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003148371-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1061
ID ADH60662 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004023331-A1.
PA (DESN/) DESNOVERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1062
ID ADJ99719 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003187238-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1063
ID ADL08912 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003186358-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1064
ID ADM25253 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003096233-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1065
ID ADM30003 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003190611-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1066
ID ADO06325 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US6686451-B1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1067
ID ADR11177 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004137561-A1.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1068
ID ADRI8086 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004147017-A1.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOVERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOM/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYN/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1069
ID ADS74725 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004185531-A1.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOVERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
```

```

PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERK/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match 12.4%; Score 224; DB 8; Length 1059;
  Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1070
ID ADT03762 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 8; Length 1059;
  Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1071
ID AEA38000 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 9; Length 1059;
  Best Local Similarity 23.9%; Pred. No. 6.6e-10;
RESULT 1072
ID AAY08114 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 2; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1073
ID AAY70674 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 3; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1074
ID ADC78606 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1075
ID AAB80263 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 4; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1076
ID AAB48162 standard; protein; 1119 AA.
DE Human PRO326 polypeptide.
PN WO200075316-A1.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1077
ID AAU00827 standard; protein; 1119 AA.
DE Human immune response protein PRO326 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 4; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1078
ID AAU12347 standard; protein; 1119 AA.
DE Human PRO326 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 4; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1079
ID ABU71641 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1080
ID AB017791 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1081
ID ABU71496 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1082
ID ABU81045 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1083
ID ABU71942 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1084
ID ABO01825 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match 12.4%; Score 224; DB 6; Length 1119;
  Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1085
ID ABU66745 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003036180-A1.
PD 20-FEB-2003.

```

```
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1086
ID ABUS4398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US200213240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1087
ID ABO47413 standard; protein; 1119 AA.
DE Human secreted/transmembrane polypeptide PRO326.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1088
ID ABUS9826 standard; protein; 1119 AA.
DE Novel secreted and transmembrane protein PRO326.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1089
ID ABO25016 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein (PRO) #176.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1090
ID ABUS4550 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #54.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1091
ID ABUS67396 standard; protein; 1119 AA.
DE Human secreted protein PRO326.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1092
ID ABO44916 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1093
ID ABUS67021 standard; protein; 1119 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 352.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1094
ID ABUS9673 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1095
ID ABO14855 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1096
ID ADA45871 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1097
ID ADA76302 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1098
ID ADB29499 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1099
ID ADA18952 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1100
ID ADA61575 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1101
ID ADB19360 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1102
ID ADB27901 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1103
ID ADA86380 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
```

Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1104
ID ADB15944 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1105
ID ADA47730 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1106
ID ADA18355 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1107
ID ABO32807 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1108
ID ABO32808 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO332.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1109
ID ADA67525 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1110
ID ADB30532 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1111
ID ADA85828 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1112
ID ADA97040 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;

RESULT 1113
ID ADA79344 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1114
ID ADA87483 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1115
ID ADB16685 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1116
ID ABO34867 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1117
ID ADA16330 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1118
ID ADA91777 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1119
ID ADB14840 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1120
ID ADB18801 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1121
ID ADA94016 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1122
ID ADA97040 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;

```

ID ADB19912 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1123
ID ADB13224 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1124
ID ABO43324 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1125
ID ADA74478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1126
ID ADA42475 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1127
ID ADB24711 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1128
ID ADA82235 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1129
ID ADA75198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1130
ID ADA85276 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1131
ID ADA84724 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1132
ID ABO17545 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1133
ID ADB29980 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1134
ID ADA80508 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1135
ID ADA75750 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1136
ID ADA46975 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1137
ID ADB25271 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1138
ID ADA93447 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1139
ID ADB26797 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1140
ID ADB31084 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
```



```
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1141
ID ADA61012 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1142
ID ADB24159 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1143
ID ADA96488 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1144
ID ADA81060 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1145
ID ADA95936 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1146
ID ADB26245 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1147
ID ADB21730 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1148
ID ADA77509 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1149
ID ADB18249 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1150
ID ADA86932 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1151
ID ADA16754 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1152
ID ADA13183 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1153
ID ADA42051 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1154
ID ADA88035 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1155
ID ADA48423 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1156
ID ADA17398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1157
ID ADA42901 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1158
ID ADB28453 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082699-A1.
PD 01-MAY-2003.
```

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1159
ID ADB29005 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1160
ID ADA76957 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1161
ID ADA88587 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1162
ID ADA97592 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1163
ID ADB27349 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200302239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1164
ID ADB22282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1165
ID ABO17606 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1166
ID ADA66973 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1167
ID ADB22834 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;

RESULT 1168
ID ADB23607 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077112-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1169
ID ADA92329 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1170
ID ADB15392 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1171
ID ADB36644 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1172
ID ADB38092 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1173
ID ADB66564 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1174
ID ADB89644 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1175
ID ADB90376 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1176
ID ADB77820 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1177
ID ADB77820 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;

ID ADB39477 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1178
ID ADB74956 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1179
ID ADB47100 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1180
ID ADB86707 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1181
ID ADB77312 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1182
ID ADB34469 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1183
ID ADB35573 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1184
ID ADB33917 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1185
ID ADB35021 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1186
ID ADB36125 standard; protein; 1119 AA.

DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1187
ID ADB46520 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1188
ID ADC28602 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1189
ID ADC39802 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1190
ID ADC40316 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1191
ID ADC19140 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1192
ID ADC34440 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1193
ID ADC29495 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1194
ID ADC29026 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1195
ID ADC40911 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.

PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1196
ID ADC19568 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1197
ID ADC34016 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1198
ID ADC13086 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1199
ID ADC50393 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1200
ID ADC71940 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1201
ID ADC59919 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1202
ID ADC52926 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1203
ID ADC37280 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1204
ID ADC60471 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087367-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1205
ID ADC50946 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1206
ID ADC65473 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1207
ID ADC54571 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1208
ID ADC53532 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1209
ID ADC59055 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1210
ID ADC55933 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1211
ID ADC58503 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1212
ID ADC12538 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1213
ID ADD03177 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092104-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1214
ID ADC90169 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1215
ID ADC69588 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1216
ID ADC48477 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1217
ID ADD10006 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1218
ID ADD04581 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1219
ID ADC80537 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1220
ID ADD11044 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1221
ID ADC47925 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1222
ID ADD05093 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1223
ID ADC79985 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1224
ID ADD09454 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1225
ID ADD04099 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1226
ID ADD03675 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1227
ID ADD41167 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1228
ID ADD52306 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1229
ID ADD53046 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1230
ID ADD53598 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1231
ID ADD51754 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1232
ID ADD05093 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

```
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1232
ID ADD02553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1233
ID ADD01987 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1234
ID ADD54169 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1235
ID ADD92486 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1236
ID ADD91382 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1237
ID ADE031996 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1238
ID ADE32293 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1239
ID ADE22225 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1240
ID ADD79449 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1241
ID ADE41985 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1242
ID ADE17802 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1243
ID ADD91934 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1244
ID ADE33397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1245
ID ADE33949 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1246
ID ADD80001 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1247
ID ADD93038 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1248
ID ADE19458 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1249
ID ADE34927 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1250
```

ID ADE18906 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1251
ID ADE43102 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1252
ID ADD95891 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1253
ID ADE22777 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1254
ID ADD78895 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1255
ID ADE32845 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1256
ID ADE42537 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1257
ID ADD80553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1258
ID ADD89581 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1259
ID ADE40865 standard; protein; 1119 AA.

DE Human PRO polypeptide #176.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1260
ID ADE04664 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1261
ID ADE92793 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1262
ID ADG21502 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1263
ID ADG23143 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1264
ID ADF97478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1265
ID ADG80542 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1266
ID ADG79990 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1267
ID ADH59410 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1268
ID ADH55282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.

PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1269
ID ADH55834 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1270
ID ADI38189 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1271
ID ADI64053 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1272
ID ADI65002 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1273
ID ADI69501 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1274
ID ADH81915 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1275
ID ADH81363 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1276
ID ADJ26457 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1277
ID ADM82532 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087355-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1278
ID ADN15931 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1279
ID ADN16560 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1280
ID ADN15379 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1281
ID ADN14827 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1282
ID ADC81089 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1283
ID ADE79372 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1284
ID ADD76537 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1285
ID ADD87901 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1286
ID ADD86305 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203440-A1.
PD 30-OCT-2003.


```
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1287
ID ADE79796 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1298
ID ADE75753 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1289
ID ADE73472 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1290
ID ADE23329 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1291
ID ADE23881 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1292
ID ADE24524 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1293
ID ADD87349 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1294
ID ADE89215 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1295
ID ADE74007 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1296
ID ADE18354 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1297
ID ADE8663 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1298
ID ADE99561 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1299
ID ADE94683 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1300
ID ADE91094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1301
ID ADE95235 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1302
ID ADE93345 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1303
ID ADF34926 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1304
ID ADE98680 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
```

Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1305
ID ADE92241 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1306
ID ADE90542 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1307
ID ADE91689 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1308
ID ADE99107 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1309
ID ADG40577 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1310
ID ADF73971 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1311
ID ADG02268 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1312
ID ADG22054 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1313
ID ADG20124 standard; protein; 1119 AA.

DE Human PRO polypeptide #176.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1314
ID ADF98030 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1315
ID ADG24247 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1316
ID ADF98601 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1317
ID ADG03432 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1318
ID ADF99153 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1319
ID ADG16738 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1320
ID ADG05197 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1321
ID ADG19464 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1322
ID ADF73547 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.

```
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1323
ID ADG13301 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1324
ID ADG08358 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1325
ID ADG15528 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1326
ID ADF96926 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1327
ID ADG06111 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1328
ID ADG23695 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1329
ID ADG03984 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1330
ID ADG24885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1331
ID ADG07182 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207350-A1.
PD 06-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1332
ID ADG07734 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1333
ID ADG5229 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1334
ID ADG60893 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1335
ID ADG61997 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1336
ID ADG92390 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1337
ID ADG82198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1338
ID ADG57437 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1339
ID ADG56885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1340
ID ADG55781 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207365-A1.
PD 06-NOV-2003.
```

```
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1341
ID ADG58541 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1342
ID ADG70907 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1343
ID ADG92817 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003207146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1344
ID ADG57989 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1345
ID ADG33573 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1346
ID ADG71459 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1347
ID ADG81646 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1348
ID ADH30608 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1349
ID ADH11975 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1350
ID ADG52397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1351
ID ADG54125 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1352
ID ADG81094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1353
ID ADG56333 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1354
ID ADH12599 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1355
ID ADG61445 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1356
ID ADH28532 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1357
ID ADG54677 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1358
ID ADG59717 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
```



```
RESULT 1375
ID ADL08916 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003186359-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1376
ID ADM25257 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1377
ID ADJ63563 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1378
ID ADM30007 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1379
ID ADJ77458 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1380
ID ADJ65580 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1381
ID ADM27716 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1382
ID ADM42440 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1383
ID ADO06329 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1384
ID ADM28302 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1385
ID ADR1181 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1386
ID ADR18090 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN J J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1387
ID ADI95784 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1388
ID ADI96336 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 7.2e-10;
RESULT 1389
ID ADS74729 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein #56.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
```


Best Local Similarity 24.8%; Pred. No. 9.4e-10;
RESULT 1403
ID ADR09753 standard; protein; 595 AA.
DE Human protein useful for treating neurological disease Seq 3259.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.3%; Score 222; DB 8; Length 595;
Best Local Similarity 27.2%; Pred. No. 4.5e-10;
RESULT 1404
ID ABB10202 standard; protein; 744 AA.
DE Human cDNA SEQ ID NO: 510.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.3%; Score 222; DB 4; Length 744;
Best Local Similarity 23.6%; Pred. No. 6.1e-10;
RESULT 1405
ID ABP66789 standard; protein; 744 AA.
DE Human polypeptide SEQ ID NO 510.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 12.3%; Score 222; DB 5; Length 744;
Best Local Similarity 23.8%; Pred. No. 6.1e-10;
RESULT 1406
ID ADH72194 standard; protein; 1068 AA.
DE Human protein of the invention NOV51d SEQ ID NO:1090.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.3%; Score 222; DB 8; Length 1068;
Best Local Similarity 24.2%; Pred. No. 1e-09;
RESULT 1407
ID AAW42087 standard; protein; 1571 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM2.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match 12.2%; Score 221; DB 2; Length 1571;
Best Local Similarity 28.6%; Pred. No. 2.1e-09;
RESULT 1408
ID AAW42086 standard; protein; 1910 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM1.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match 12.2%; Score 221; DB 2; Length 1910;
Best Local Similarity 28.6%; Pred. No. 2.7e-09;
RESULT 1409
ID ADK71092 standard; protein; 2012 AA.
DE Human MP21 polypeptide.
PN WO2004015073-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 12.2%; Score 221; DB 8; Length 2012;
Best Local Similarity 28.6%; Pred. No. 2.9e-09;
RESULT 1410
ID AAB35586 standard; protein; 364 AA.
DE Protein encoded by human secreted protein gene #11.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.2%; Score 220.5; DB 3; Length 364;
Best Local Similarity 26.0%; Pred. No. 3.1e-10;
RESULT 1411
ID ADA27058 standard; protein; 364 AA.
DE Human novel secreted protein from cDNA HOUDJ81 #1.
PN US2003055231-A1.
PD 20-MAR-2003.
PA (NIJ/) NI J.
Query Match 12.2%; Score 220.5; DB 2; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.1e-10;
RESULT 1412
ID ADE86588 standard; protein; 364 AA.
DE Novel human secreted protein #11.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KINN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREG/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROC/) CROCKER P R.
Query Match 12.2%; Score 220.5; DB 6; Length 364;
Best Local Similarity 26.0%; Pred. No. 3.1e-10;
RESULT 1413
ID ADR41469 standard; protein; 370 AA.
DE Human CD-like molecule HATCZ07, SEQ ID NO:268.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.2%; Score 220.5; DB 5; Length 370;
Best Local Similarity 26.0%; Pred. No. 3.2e-10;
RESULT 1414
ID AAM23691 standard; protein; 402 AA.
DE Human EST encoded protein SEQ ID NO: 1216.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.2%; Score 220.5; DB 4; Length 402;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1415
ID AAY45093 standard; protein; 423 AA.
DE Mouse lymphoid derived dendritic cell adhesion molecule.
PN WO200008158-A2.
PD 17-FEB-2000.
PA (IMV) IMMUNEX CORP.
Query Match 12.2%; Score 220.5; DB 3; Length 423;
Best Local Similarity 26.0%; Pred. No. 3.8e-10;
RESULT 1416
ID ADW91678 standard; protein; 423 AA.
DE Mouse LdCAM.
PN WO2005012530-A2.
PD 10-FEB-2005.
PA (AMGE-) AMGEN INC.
Query Match 12.2%; Score 220.5; DB 9; Length 423;
Best Local Similarity 26.0%; Pred. No. 3.8e-10;
RESULT 1417
ID ABO84564 standard; protein; 425 AA.
DE Human cancer-associated protein HP16-039.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.2%; Score 220.5; DB 8; Length 425;
Best Local Similarity 26.0%; Pred. No. 3.8e-10;
RESULT 1418
ID AAY17830 standard; protein; 440 AA.
DE Human PRO355 protein sequence.
PN WO9928462-A2.
PD 10-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 2; Length 440;

Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1419			RESULT 1429		
ID AAB01321 standard; protein; 440 AA.			ID ABU89843 standard; protein; 440 AA.		
DE Human PRO355 polypeptide.			DE Novel human secreted and transmembrane protein PRO355.		
PN W020032776-A2.			PN US2003036147-A1.		
PD 08-JUN-2000.			PD 20-FEB-2003.		
PA (GETH) GENENTECH INC.			Query Match	12.2%;	Score 220.5; DB 3; Length 440;
Best Local Similarity	12.2%;	Score 220.5; DB 3; Length 440;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1420			RESULT 1430		
ID AAU29040 standard; protein; 440 AA.			ID ABR68092 standard; protein; 440 AA.		
DE Human PRO polypeptide sequence #17.			DE Human secreted polypeptide PRO355, SEQ ID NO:34.		
PN W0200168848-A2.			PN US2003027264-A1.		
PD 20-SEP-2001.			PD 06-FEB-2003.		
PA (GETH) GENENTECH INC.			Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	12.2%;	Score 220.5; DB 4; Length 440;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1421			RESULT 1431		
ID ABUS8416 standard; protein; 440 AA.			ID ABU96145 standard; protein; 440 AA.		
DE Human PRO polypeptide #17.			DE Novel human secreted and transmembrane protein PRO355.		
PN US2003027272-A1.			PN US2003036144-A1.		
PD 06-FEB-2003.			PD 20-FEB-2003.		
Query Match	12.2%;	Score 220.5; DB 6; Length 440;	Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1422			RESULT 1432		
ID ABU87964 standard; protein; 440 AA.			ID ABU92576 standard; protein; 440 AA.		
DE Novel human secreted and transmembrane protein PRO355.			DE Human secreted/transmembrane protein (PRO) #17.		
PN US2003032127-A1.			PN US2003036149-A1.		
PD 13-FEB-2003.			PD 20-FEB-2003.		
Query Match	12.2%;	Score 220.5; DB 6; Length 440;	Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1423			RESULT 1433		
ID ABU84279 standard; protein; 440 AA.			ID ABO08653 standard; protein; 440 AA.		
DE Human secreted/transmembrane protein (PRO) #17.			DE Human secreted/transmembrane protein (PRO) #17.		
PN US2003032112-A1.			PN US2003044923-A1.		
PD 13-FEB-2003.			PD 06-MAR-2003.		
Query Match	12.2%;	Score 220.5; DB 6; Length 440;	Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1424			RESULT 1434		
ID ABR66153 standard; protein; 440 AA.			ID ABO02705 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO355, SEQ ID NO:34.			DE Human secreted/transmembrane protein (PRO) #17.		
PN US2003027278-A1.			PN US2003040062-A1.		
PD 06-FEB-2003.			PD 27-FEB-2003.		
Query Match	12.2%;	Score 220.5; DB 6; Length 440;	Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1425			RESULT 1435		
ID ABR65543 standard; protein; 440 AA.			ID ABR74859 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO355, SEQ ID NO:34.			DE Human secreted polypeptide PRO355, SEQ ID NO:34.		
PN US2003036159-A1.			PN US2003040056-A1.		
PD 20-FEB-2003.			PD 27-FEB-2003.		
Query Match	12.2%;	Score 220.5; DB 6; Length 440;	Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1426			RESULT 1436		
ID ABU99483 standard; protein; 440 AA.			ID ABR94621 standard; protein; 440 AA.		
DE Human secreted/transmembrane protein (PRO) #17..			DE Human secreted polypeptide PRO355, SEQ ID NO:34.		
PN US2003040070-A1.			PN US2003044926-A1.		
PD 27-FEB-2003.			PD 06-MAR-2003.		
Query Match	12.2%;	Score 220.5; DB 6; Length 440;	Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1427			RESULT 1437		
ID ABUS5930 standard; protein; 440 AA.			ID ABU60240 standard; protein; 440 AA.		
DE Human secreted/transmembrane protein PRO355.			DE Human PRO polypeptide #11.		
PN US2002142959-A1.			PN US2002132768-A1.		
PD 03-OCT-2002.			PD 19-SEP-2002.		
PA (GETH) GENENTECH INC.			PA (GETH) GENENTECH INC.		
Query Match	12.2%;	Score 220.5; DB 6; Length 440;	Query Match	12.2%;	Score 220.5; DB 6; Length 440;
Best Local Similarity	26.0%;	Pred. No. 4e-10;	Best Local Similarity	26.0%;	Pred. No. 4e-10;
RESULT 1428					

RESULT 1439
ID ABU98754 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1440
ID ABU97969 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1441
ID ABU91675 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1442
ID ABU9368 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1443
ID ABU86209 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036146-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1444
ID ABU67422 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1445
ID ABU80450 standard; protein; 440 AA.
DE Human PRO protein #17.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1446
ID ABR99368 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1447
ID ABR98758 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1448
ID ABO16281 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;

RESULT 1449
ID ABR22181 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1450
ID ABO18922 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1451
ID ABR78243 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1452
ID ABU64926 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO355.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1453
ID ABU84979 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1454
ID ABO00118 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1455
ID ABO11450 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1456
ID ABO02095 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1457
ID ABU58360 standard; protein; 440 AA.
DE Novel human secreted protein PRO355.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1458
ID ABU88669 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;

RESULT 1459
ID ABU83364 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036134-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1460
ID ABO06165 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003022294-A1.
PD 30-JAN-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1461
ID ABR59201 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027275-A1.
PD 06-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1462
ID ABO0263 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027324-A1.
PD 06-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1463
ID ABO19127 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036118-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1464
ID ABO11145 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036123-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1465
ID ABR66763 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036148-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1466
ID ABO15976 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040060-A1.
PD 27-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1467
ID ABO13682 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044916-A1.
PD 06-MAR-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1468
ID ABU57246 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2002142958-A1.
PD 03-OCT-2002. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1469
ID ABR69979 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036143-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1470
ID ABO07433 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032117-A1.
PD 13-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1471
ID ABO03620 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036128-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1472
ID ABR67068 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027266-A1.
PD 06-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1473
ID ABO15671 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003054483-A1.
PD 20-MAR-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1474
ID ABU55952 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.
PN US2003022298-A1.
PD 30-JAN-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1475
ID ABU65280 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032102-A1.
PD 13-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1476
ID ABU95225 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036117-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1477
ID ABU71128 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2003036143-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1478
ID ABO07738 standard; protein; 440 AA.
DE Human-PRO polypeptide #17.
PN US2003032130-A1.
PD 13-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1479
ID ABR69979 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036143-A1.
PD 20-FEB-2003. 12.2%; Score 220.5; DB 6; Length 440;
Query Match 26.0%; Pred. No. 4e-10;
Best Local Similarity 26.0%; Pred. No. 4e-10;

PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1480
ID ABR69312 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1481
ID ABO01453 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1482
ID ABU81255 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1483
ID ABR60052 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1484
ID ABR67787 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1485
ID ABR65175 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027288-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1486
ID ABR68397 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1487
ID ABR71809 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1488
ID ABU85289 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1489
ID ABU88979 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.

PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1490
ID ABU83059 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1491
ID ABU94915 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1492
ID ABU90463 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1493
ID ABU83974 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1494
ID ABU93625 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1495
ID ABR64870 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1496
ID ABR68702 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1497
ID ABO06518 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1498
ID ABR99063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 1499
ID ABUS6311 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.
PN US2002132981-A1.
PD 19-SEP-2002.

PA (GETH) GENENTECH INC.
 Query Match 12.2%; Score 220.5; DB 6; Length 440;
 Best Local Similarity 26.0%; Pred. No. 4e-10;
 RESULT 1500
 ID ABUS6947 standard; protein; 440 AA.
 DE Human PRO polypeptide #17.
 FN US2003027280-A1.
 PD 06-FEB-2003.
 Query Match 12.2%; Score 220.5; DB 6; Length 440;
 Best Local Similarity 26.0%; Pred. No. 4e-10;

This Page Blank (uspto)

101	220.5	12.2	440	2	US-09-944-944-61	Sequence 61, Appl	174	192.5	10.7	985	2	US-09-877-730-10	Sequence 10, Appl
102	220.5	12.2	440	2	US-09-945-587-61	Sequence 61, Appl	175	192.5	10.7	991	2	US-09-877-730-12	Sequence 12, Appl
103	220.5	12.2	442	2	US-09-778-510-20	Sequence 20, Appl	176	192.5	10.7	1069	2	US-09-877-730-2	Sequence 2, Appl
104	220.5	12.2	442	2	US-09-330-803-1	Sequence 1, Appl	177	192.5	10.7	1072	2	US-09-877-730-18	Sequence 18, Appl
105	219	12.1	1091	2	US-08-986-485-5	Sequence 5, Appl	178	192.5	10.7	1150	2	US-09-877-730-8	Sequence 8, Appl
106	219	12.1	1101	2	US-08-986-485-2	Sequence 2, Appl	179	192.5	10.7	1260	2	US-08-506-296B-21	Sequence 21, Appl
107	218.5	12.1	1115	2	US-10-012-231A-58	Sequence 58, Appl	180	192.5	10.7	1268	2	US-08-506-296B-28	Sequence 28, Appl
108	218.5	12.1	1115	2	US-10-015-389A-58	Sequence 58, Appl	181	192	10.6	529	2	US-09-383-586-31	Sequence 31, Appl
109	218.5	12.1	1115	2	US-10-006-768A-58	Sequence 58, Appl	182	192	10.6	529	2	US-09-823-038A-31	Sequence 31, Appl
110	218.5	12.1	1115	2	US-10-015-671A-58	Sequence 58, Appl	183	192	10.6	650	2	US-10-104-047-3395	Sequence 3395, Ap
111	218.5	12.1	1115	2	US-10-015-393A-58	Sequence 58, Appl	184	191.5	10.6	1209	2	US-09-130-158A-2	Sequence 2, Appl
112	218.5	12.1	1115	2	US-10-011-833A-58	Sequence 58, Appl	185	188.5	10.4	651	2	US-09-270-767-44877	Sequence 44877, A
113	218.5	12.1	1115	2	US-10-006-041A-58	Sequence 58, Appl	186	187.5	10.4	1266	2	US-08-506-296B-4	Sequence 4, Appl
114	218.5	12.1	1115	2	US-10-012-064A-58	Sequence 58, Appl	187	185.5	10.3	318	1	US-08-633-148-4	Sequence 4, Appl
115	213.5	11.8	398	2	US-09-778-510-6	Sequence 6, Appl	188	185.5	10.3	332	2	US-09-062-365-1	Sequence 1, Appl
116	213.5	11.8	398	2	US-09-507-794A-84	Sequence 84, Appl	189	185.5	10.3	339	2	US-09-799-152-2	Sequence 2, Appl
117	213.5	11.8	398	2	US-09-905-125A-84	Sequence 84, Appl	190	185.5	10.3	340	1	US-08-633-148-2	Sequence 2, Appl
118	213.5	11.8	398	2	US-09-902-775A-84	Sequence 84, Appl	191	185.5	10.3	404	2	US-09-949-016-11025	Sequence 11025, A
119	213.5	11.8	398	2	US-09-906-700-84	Sequence 84, Appl	192	185.5	10.3	404	2	US-09-799-152-1	Sequence 1, Appl
120	213.5	11.8	398	2	US-09-903-603A-84	Sequence 84, Appl	193	185.5	10.3	642	1	US-08-217-239-1	Sequence 1, Appl
121	213.5	11.8	398	2	US-09-904-920A-84	Sequence 84, Appl	194	185.5	10.3	698	1	US-08-602-725-36	Sequence 36, Appl
122	213.5	11.8	398	2	US-09-909-064-84	Sequence 84, Appl	195	185.5	10.3	702	2	US-09-949-016-6484	Sequence 6484, Ap
123	213.5	11.8	398	2	US-09-905-381A-84	Sequence 84, Appl	196	185.5	10.3	734	1	US-08-389-459A-17	Sequence 17, Appl
124	213.5	11.8	398	2	US-09-906-618-84	Sequence 84, Appl	197	185.5	10.3	734	1	US-08-987-867A-17	Sequence 17, Appl
125	213.5	11.8	398	2	US-09-906-646-84	Sequence 84, Appl	198	185.5	10.3	740	2	US-09-949-016-8168	Sequence 8168, Ap
126	213.5	11.8	398	2	US-09-904-462-84	Sequence 84, Appl	199	185	10.2	1381	2	US-09-540-245A-16	Sequence 16, Appl
127	213.5	11.8	398	2	US-09-902-736A-84	Sequence 84, Appl	200	185	10.2	1381	2	US-10-289-776-16	Sequence 16, Appl
128	213.5	11.8	398	2	US-09-906-722A-84	Sequence 84, Appl	201	185	10.2	2596	2	US-09-548-473B-6	Sequence 6, Appl
129	213	11.7	59	1	US-08-414-657D-52	Sequence 52, Appl	202	184.5	10.2	66	1	US-08-414-657D-54	Sequence 54, Appl
130	212	11.7	59	1	US-08-414-657D-53	Sequence 53, Appl	203	184.5	10.2	66	1	US-08-414-657D-55	Sequence 55, Appl
131	211.5	11.7	1070	2	US-09-961-403-3	Sequence 3, Appl	204	184.5	10.2	404	2	US-09-638-649-3	Sequence 3, Appl
132	211.5	11.7	1461	2	US-09-976-594-531	Sequence 531, App	205	184.5	10.2	404	2	US-09-638-648-3	Sequence 3, Appl
133	211	11.7	398	2	US-09-778-510-4	Sequence 4, Appl	206	184	10.2	373	2	US-09-823-038A-60	Sequence 60, Appl
134	211	11.7	615	1	US-08-752-307B-9	Sequence 9, Appl	207	184	10.2	426	2	US-08-755-235-4	Sequence 4, Appl
135	211	11.7	615	2	US-09-707-802-9	Sequence 9, Appl	208	182	10.1	626	2	US-09-949-016-6213	Sequence 6213, Ap
136	211	11.7	615	2	US-09-991-326-9	Sequence 9, Appl	209	182	10.1	664	2	US-09-949-016-7850	Sequence 7850, Ap
137	210	11.6	191	2	US-09-270-767-32640	Sequence 9, Appl	210	181	10.0	885	2	US-10-104-047-2946	Sequence 2946, Ap
138	210	11.6	1953	2	US-09-917-254-92	Sequence 92, Appl	211	179	9.9	300	2	US-09-254-465A-10	Sequence 10, Appl
139	209	11.6	504	2	US-09-949-016-7020	Sequence 7020, Ap	212	179	9.9	300	2	US-09-993-439D-12	Sequence 12, Appl
140	209	11.6	504	2	US-09-991-181-119	Sequence 119, App	213	179	9.9	300	2	US-09-953-499-10	Sequence 10, Appl
141	209	11.6	504	2	US-09-990-444-119	Sequence 119, App	214	174	9.6	261	2	US-09-270-767-32898	Sequence 32898, A
142	209	11.6	504	2	US-09-997-333-119	Sequence 119, App	215	174	9.6	261	2	US-09-270-767-48115	Sequence 48115, A
143	209	11.6	504	2	US-09-992-598-119	Sequence 119, App	216	173.5	9.6	544	2	US-09-999-833A-259	Sequence 259, App
144	209	11.6	511	2	US-09-949-016-10054	Sequence 10054, A	217	173.5	9.6	544	2	US-10-020-445A-259	Sequence 259, App
145	208.5	11.5	1651	2	US-09-940-245A-18	Sequence 18, Appl	218	171.5	9.5	780	1	US-08-232-538-14	Sequence 14, Appl
146	208.5	11.5	1651	2	US-10-289-776-18	Sequence 18, Appl	219	171.5	9.5	780	1	US-08-786-164-14	Sequence 14, Appl
147	207.5	11.5	329	2	US-10-104-047-3709	Sequence 3709, Ap	220	171.5	9.5	1338	2	US-08-750-141A-3	Sequence 3, Appl
148	205.5	11.4	596	1	US-08-752-307B-13	Sequence 13, Appl	221	171.5	9.5	1338	2	US-09-119-014D-6	Sequence 6, Appl
149	205.5	11.4	596	2	US-09-707-802-13	Sequence 13, Appl	222	171	9.5	464	1	US-08-602-725-32	Sequence 32, Appl
150	205.5	11.4	596	2	US-09-991-326-13	Sequence 13, Appl	223	171	9.5	464	2	US-09-949-016-6116	Sequence 6116, Ap
151	205	11.4	432	4	PCT-US95-510-2	Sequence 2, Appl	224	171	9.5	464	2	US-09-949-016-7525	Sequence 7525, Ap
152	201	11.1	946	4	PCT-US95-08493-13	Sequence 13, Appl	225	171	9.5	917	1	US-08-245-295-2	Sequence 2, Appl
153	199	11.0	1241	2	US-09-040-774-2	Sequence 2, Appl	226	171	9.5	917	1	US-08-481-130-2	Sequence 2, Appl
154	198	11.0	847	2	US-09-949-002-328	Sequence 328, App	227	171	9.5	917	1	US-08-656-984A-2	Sequence 2, Appl
155	198	11.0	862	2	US-09-949-002-427	Sequence 427, App	228	171	9.5	917	1	US-08-485-604-2	Sequence 2, Appl
156	198	11.0	1709	2	US-09-949-016-10503	Sequence 10503, A	229	171	9.5	917	1	US-08-487-595-2	Sequence 2, Appl
157	197.5	10.9	1447	2	US-09-041-886-25	Sequence 25, Appl	230	171	9.5	1253	2	US-08-506-296B-14	Sequence 14, Appl
158	197.5	10.9	1447	4	PCT-US94-05277-2	Sequence 2, Appl	231	170	9.4	318	2	US-09-068-051A-32	Sequence 32, Appl
159	197	10.9	1297	2	US-09-540-245A-17	Sequence 17, Appl	232	167.5	9.3	280	2	US-09-270-767-43068	Sequence 43068, A
160	197	10.9	1297	2	US-10-289-776-17	Sequence 17, Appl	233	167.5	9.3	466	1	US-08-432-016-4	Sequence 4, Appl
161	196.5	10.9	833	2	US-09-949-016-11496	Sequence 11496, A	234	167.5	9.3	466	1	US-08-684-594-4	Sequence 4, Appl
162	196.5	10.9	1180	2	US-09-949-016-6577	Sequence 6577, Ap	235	167	9.2	668	1	US-08-232-538-13	Sequence 13, Appl
163	195.5	10.8	619	2	US-10-104-047-2048	Sequence 2048, Ap	236	167	9.2	668	1	US-08-786-164-13	Sequence 13, Appl
164	195	10.8	630	1	US-08-752-307B-14	Sequence 14, Appl	237	167	9.2	764	2	US-09-142-956B-14	Sequence 14, Appl
165	195	10.8	630	2	US-09-707-802-14	Sequence 14, Appl	238	167	9.2	767	1	US-08-874-678-2	Sequence 2, Appl
166	195	10.8	630	2	US-09-991-326-14	Sequence 14, Appl	239	167	9.2	767	1	US-08-643-839-2	Sequence 2, Appl
167	192.5	10.7	612	1	US-08-752-307B-11	Sequence 11, Appl	240	167	9.2	767	2	US-09-348-886-2	Sequence 2, Appl
168	192.5	10.7	612	2	US-09-707-802-11	Sequence 11, Appl	241	167	9.2	767	2	US-10-105-901A-2	Sequence 2, Appl
169	192.5	10.7	612	2	US-09-991-326-11	Sequence 11, Appl	242	167	9.2	788	1	US-08-232-538-15	Sequence 15, Appl
170	192.5	10.7	826	2	US-09-877-730-16	Sequence 16, Appl	243	167	9.2	788	1	US-08-786-164-15	Sequence 15, Appl
171	192.5	10.7	904	2	US-09-877-730-6	Sequence 6, Appl	244	167	9.2	1356	1	US-08-810-116-8	Sequence 8, Appl
172	192.5	10.7	907	2	US-09-877-730-20	Sequence 20, Appl	245	167	9.2	1356	1	US-07-930-548A-8	Sequence 8, Appl
173	192.5	10.7	983	2	US-09-412-554A-2	Sequence 2, Appl	246	167	9.2	1356	2	US-09-098-707A-2	Sequence 2, Appl

247	167	9.2	1356	2	US-09-483-539-2	Sequence 2, Appli	320	160	8.9	270	2	US-09-254-465A-24	Sequence 24, Appl
248	167	9.2	1356	2	US-09-949-016-6198	Sequence 6198, Ap	321	160	8.9	270	2	US-09-953-499-24	Sequence 24, Appl
249	167	9.2	1356	2	US-10-100-405A-2	Sequence 2, Appli	322	160	8.9	273	2	US-09-254-465A-26	Sequence 26, Appl
250	167	9.2	1356	2	US-10-022-939-2	Sequence 2, Appli	323	160	8.9	273	2	US-09-953-499-26	Sequence 26, Appl
251	167	9.2	1456	2	US-09-949-016-9853	Sequence 9853, Ap	324	160	8.9	319	1	US-08-597-495B-22	Sequence 22, Appl
252	166.5	9.2	302	2	US-09-877-730-14	Sequence 14, Appli	325	160	8.9	319	2	US-09-068-051A-22	Sequence 22, Appl
253	166.5	9.2	380	2	US-09-877-730-4	Sequence 4, Appli	326	160	8.9	319	2	US-09-336-536-67	Sequence 67, Appl
254	166	9.2	758	1	US-08-874-678-1	Sequence 1, Appli	327	160	8.9	319	2	US-09-254-465A-6	Sequence 6, Appli
255	166	9.2	758	2	US-08-643-839-1	Sequence 1, Appli	328	160	8.9	319	2	US-09-953-499-6	Sequence 6, Appli
256	166	9.2	758	2	US-09-051-363-24	Sequence 24, Appli	329	160	8.9	609	2	US-09-949-016-7747	Sequence 7747, Ap
257	166	9.2	758	2	US-09-348-886-1	Sequence 1, Appli	330	160	8.9	609	2	US-09-949-016-7748	Sequence 7748, Ap
258	166	9.2	758	2	US-10-105-901A-1	Sequence 1, Appli	331	160	8.9	609	2	US-09-949-016-7749	Sequence 7749, Ap
259	165.5	9.2	758	1	US-08-432-016-5	Sequence 5, Appli	332	160	8.9	609	2	US-09-949-016-7750	Sequence 7750, Ap
260	165.5	9.2	278	1	US-08-684-594-5	Sequence 5, Appli	333	160	8.9	609	2	US-09-949-016-7751	Sequence 7751, Ap
261	165.5	9.2	486	1	US-08-432-016-6	Sequence 6, Appli	334	160	8.9	609	2	US-09-949-016-7752	Sequence 7752, Ap
262	165.5	9.2	486	1	US-08-684-594-6	Sequence 6, Appli	335	160	8.9	609	2	US-09-949-016-7753	Sequence 7753, Ap
263	165.5	9.2	583	1	US-08-432-016-2	Sequence 2, Appli	336	160	8.9	609	2	US-09-949-016-7754	Sequence 7754, Ap
264	165.5	9.2	583	1	US-08-684-594-2	Sequence 2, Appli	337	160	8.9	817	1	US-07-640-029-2	Sequence 2, Appli
265	165.5	9.2	646	2	US-09-949-016-6728	Sequence 6728, Ap	338	160	8.9	822	1	US-07-921-807B-4	Sequence 4, Appli
266	165.5	9.2	646	2	US-09-653-961-4	Sequence 4, Appli	339	160	8.9	822	1	US-08-459-296-2	Sequence 2, Appli
267	165.5	9.2	828	1	US-08-361-304-2	Sequence 2, Appli	340	160	8.9	822	1	US-08-441-944A-4	Sequence 4, Appli
268	165.5	9.2	1617	2	US-09-784-358-16	Sequence 16, Appli	341	160	8.9	822	1	US-08-451-822A-12	Sequence 12, Appli
269	165.5	9.2	1691	2	US-09-784-358-2	Sequence 2, Appli	342	160	8.9	822	2	US-08-439-992A-2	Sequence 2, Appli
270	165	9.1	501	1	US-08-408-095-31	Sequence 31, Appli	343	160	8.9	822	2	US-08-323-430-12	Sequence 12, Appli
271	164.5	9.1	1194	2	US-10-191-029-10	Sequence 10, Appli	344	160	8.9	822	2	US-09-620-561-2	Sequence 2, Appli
272	164	9.1	439	2	US-09-383-586-32	Sequence 32, Appli	345	159	8.8	822	1	US-07-997-133-1	Sequence 1, Appli
273	164	9.1	439	2	US-09-823-038A-32	Sequence 32, Appli	346	158.5	8.8	1474	2	US-09-677-046A-4	Sequence 4, Appli
274	164	9.1	640	2	US-09-949-016-7565	Sequence 7565, Ap	347	158.5	8.8	1509	2	US-09-677-046A-2	Sequence 2, Appli
275	163.5	9.1	582	2	US-09-702-705-334	Sequence 334, App	348	158	8.7	292	2	US-09-800-729-175	Sequence 175, App
276	163.5	9.1	582	2	US-09-736-457-334	Sequence 334, App	349	158	8.7	611	1	US-08-752-307B-10	Sequence 10, Appl
277	163.5	9.1	582	2	US-09-614-124B-334	Sequence 334, App	350	158	8.7	611	2	US-09-707-802-10	Sequence 10, Appl
278	163.5	9.1	582	2	US-09-671-325-334	Sequence 334, App	351	158	8.7	611	2	US-09-991-326-10	Sequence 10, Appl
279	163.5	9.1	582	2	US-09-589-184-334	Sequence 334, App	352	158	8.7	736	4	PCT-US91-00031-15	Sequence 15, Appl
280	163.5	9.1	582	2	US-09-658-824-334	Sequence 334, App	353	157.5	8.7	1503	2	US-09-677-046A-6	Sequence 6, Appli
281	163.5	9.1	582	2	US-10-017-754-334	Sequence 334, App	354	157	8.7	260	2	US-09-254-465A-23	Sequence 23, Appl
282	163.5	9.1	582	2	US-09-651-563-334	Sequence 334, App	355	157	8.7	260	2	US-09-953-499-23	Sequence 23, Appl
283	163.5	9.1	582	2	US-09-519-642-334	Sequence 334, App	356	157	8.7	263	2	US-09-254-465A-25	Sequence 25, Appl
284	163.5	9.1	604	2	US-09-949-016-9548	Sequence 9548, Ap	357	157	8.7	263	2	US-09-953-499-25	Sequence 25, Appl
285	163.5	9.1	623	2	US-09-949-016-11206	Sequence 11206, A	358	157	8.7	263	2	US-09-188-930-331	Sequence 331, App
286	163.5	9.1	646	2	US-09-653-361-2	Sequence 2, Appli	359	157	8.7	299	2	US-09-462-270-2	Sequence 2, Appli
287	163.5	9.1	1745	2	US-09-800-729-89	Sequence 89, Appli	360	157	8.7	299	2	US-09-254-465A-1	Sequence 1, Appli
288	163	9.0	924	1	US-08-481-130-28	Sequence 28, Appli	361	157	8.7	299	2	US-09-312-283C-189	Sequence 189, App
289	163	9.0	924	1	US-08-656-984A-28	Sequence 28, Appli	362	157	8.7	299	2	US-09-312-283C-331	Sequence 331, App
290	163	9.0	924	1	US-08-485-604-28	Sequence 28, Appli	363	157	8.7	299	2	US-09-907-794A-119	Sequence 119, App
291	163	9.0	924	1	US-08-487-595-28	Sequence 28, Appli	364	157	8.7	299	2	US-09-905-125A-119	Sequence 119, App
292	162	9.0	321	6	5169835-17	Patent No. 5169835	365	157	8.7	299	2	US-09-902-775A-119	Sequence 119, App
293	161	8.9	310	2	US-09-907-794A-423	Sequence 423, App	366	157	8.7	299	2	US-09-397-243D-3	Sequence 3, Appli
294	161	8.9	310	2	US-09-905-125A-423	Sequence 423, App	367	157	8.7	299	2	US-09-906-700-119	Sequence 119, App
295	161	8.9	310	2	US-09-902-775A-423	Sequence 423, App	368	157	8.7	299	2	US-09-903-603A-119	Sequence 119, App
296	161	8.9	310	2	US-09-906-700-423	Sequence 423, App	369	157	8.7	299	2	US-09-904-920A-119	Sequence 119, App
297	161	8.9	310	2	US-09-903-603A-423	Sequence 423, App	370	157	8.7	299	2	US-09-909-064-119	Sequence 119, App
298	161	8.9	310	2	US-09-904-920A-423	Sequence 423, App	371	157	8.7	299	2	US-09-905-381A-119	Sequence 119, App
299	161	8.9	310	2	US-09-909-064-423	Sequence 423, App	372	157	8.7	299	2	US-09-906-618-119	Sequence 119, App
300	161	8.9	310	2	US-09-905-381A-423	Sequence 423, App	373	157	8.7	299	2	US-09-953-499-1	Sequence 1, Appli
301	161	8.9	310	2	US-09-906-618-423	Sequence 423, App	374	157	8.7	299	2	US-09-906-646-119	Sequence 119, App
302	161	8.9	310	2	US-09-906-646-423	Sequence 423, App	375	157	8.7	299	2	US-09-904-462-119	Sequence 119, App
303	161	8.9	310	2	US-09-904-462-423	Sequence 423, App	376	157	8.7	299	2	US-09-902-736A-119	Sequence 119, App
304	161	8.9	310	2	US-09-902-736A-423	Sequence 423, App	377	157	8.7	299	2	US-09-906-722A-119	Sequence 119, App
305	161	8.9	310	2	US-10-033-301-20	Sequence 20, Appli	378	156.5	8.7	416	2	US-09-638-649-1	Sequence 1, Appli
306	161	8.9	310	2	US-09-906-722A-423	Sequence 423, App	379	156.5	8.7	416	2	US-08-755-235-2	Sequence 2, Appli
307	161	8.9	622	2	US-09-499-846-2	Sequence 2, Appli	380	155.5	8.7	416	2	US-09-638-648-1	Sequence 1, Appli
308	161	8.9	806	1	US-08-443-861-5	Sequence 5, Appli	381	155.5	8.6	299	2	US-09-188-930-189	Sequence 189, App
309	161	8.9	806	2	US-08-193-829B-5	Sequence 5, Appli	382	155.5	8.6	880	1	US-08-445-640-10	Sequence 10, Appli
310	161	8.9	806	2	US-09-766-678-5	Sequence 5, Appli	383	155.5	8.6	880	2	US-08-470-558-10	Sequence 10, Appli
311	161	8.9	816	1	US-07-640-029-1	Sequence 1, Appli	384	155.5	8.6	880	2	US-08-447-314-10	Sequence 10, Appli
312	161	8.9	820	1	US-07-921-807B-3	Sequence 3, Appli	385	155.5	8.6	880	2	US-08-445-461-10	Sequence 10, Appli
313	161	8.9	820	1	US-08-441-944A-3	Sequence 3, Appli	386	155.5	8.6	880	2	US-09-323-490-10	Sequence 10, Appli
314	161	8.9	820	1	US-08-439-992A-1	Sequence 1, Appli	387	155	8.6	373	2	US-09-991-181-503	Sequence 503, App
315	161	8.9	820	2	US-08-620-561-1	Sequence 1, Appli	388	155	8.6	373	2	US-09-999-832A-59	Sequence 59, Appli
316	161	8.9	1367	1	US-08-443-861-2	Sequence 2, Appli	389	155	8.6	373	2	US-09-990-444-503	Sequence 503, App
317	161	8.9	1367	2	US-08-193-829B-2	Sequence 2, Appli	390	155	8.6	373	2	US-09-997-333-503	Sequence 503, App
318	161	8.9	1367	2	US-09-766-678-2	Sequence 2, Appli	391	155	8.6	373	2	US-09-992-598-503	Sequence 503, App
319	160.5	8.9	316	2	US-09-397-243D-13	Sequence 13, Appli	392	155	8.6	373	2	US-10-020-445A-59	Sequence 59, Appli

393	155	8.6	805	2	US-08-985-526-34	Sequence 34, Appl	465	150.5	8.3	349	2	US-09-924-103-4	Sequence 4, Appl1
394	155	8.6	1248	2	US-09-949-016-10595	Sequence 10595, A	467	150.5	8.3	411	2	US-08-470-339-189	Sequence 189, App
395	155	8.6	1248	2	US-09-949-016-10596	Sequence 10596, A	468	150.5	8.3	412	2	US-08-470-339-188	Sequence 188, App
396	155	8.6	1363	2	US-09-375-248-19	Sequence 19, Appl	469	150.5	8.3	422	2	US-08-467-602-324	Sequence 324, App
397	155	8.6	1367	1	US-07-813-593-4	Sequence 4, Appl1	470	150.5	8.3	422	2	US-08-411-295F-250	Sequence 250, App
398	155	8.6	1367	1	US-07-977-451-6	Sequence 6, Appl1	471	150.5	8.3	425	2	US-08-470-335-226	Sequence 226, App
399	155	8.6	1367	1	US-07-946-507-4	Sequence 4, Appl1	472	150.5	8.3	425	2	US-08-467-602-320	Sequence 320, App
400	155	8.6	1367	1	US-08-252-517-6	Sequence 6, Appl1	473	150.5	8.3	425	2	US-08-411-295F-246	Sequence 246, App
401	155	8.6	1367	1	US-07-906-397A-6	Sequence 6, Appl1	474	150.5	8.3	445	2	US-08-467-602-328	Sequence 328, App
402	155	8.6	1367	1	US-08-601-891-6	Sequence 6, Appl1	475	150.5	8.3	445	2	US-08-411-295F-254	Sequence 254, App
403	155	8.6	1367	1	US-09-021-324-6	Sequence 6, Appl1	476	150.5	8.3	456	2	US-08-467-602-366	Sequence 366, App
404	155	8.6	1367	2	US-09-872-136B-6	Sequence 6, Appl1	477	150.5	8.3	456	2	US-08-411-295F-292	Sequence 292, App
405	155	8.6	1367	2	US-09-919-408A-6	Sequence 6, Appl1	478	150.5	8.3	459	2	US-08-467-602-362	Sequence 362, App
406	155	8.6	1367	4	PCT-US92-02750-8	Sequence 8, Appl1	479	150.5	8.3	459	2	US-08-411-295F-288	Sequence 288, App
407	155	8.6	1367	4	PCT-US92-05401-6	Sequence 6, Appl1	480	150.5	8.3	479	2	US-08-467-602-370	Sequence 370, App
408	155	8.6	1367	4	PCT-US92-09893-6	Sequence 6, Appl1	481	150.5	8.3	479	2	US-08-411-295F-296	Sequence 296, App
409	154.5	8.6	306	2	US-10-191-029-12	Sequence 12, Appl	482	150.5	8.3	601	2	US-08-470-335-233	Sequence 233, App
410	154.5	8.6	462	1	US-08-752-307B-7	Sequence 7, Appl1	483	150.5	8.3	601	2	US-08-467-602-323	Sequence 323, App
411	154.5	8.6	462	2	US-09-707-802-7	Sequence 7, Appl1	484	150.5	8.3	601	2	US-08-411-295F-249	Sequence 249, App
412	154.5	8.6	462	2	US-09-991-326-7	Sequence 7, Appl1	485	150.5	8.3	604	2	US-08-470-335-227	Sequence 227, App
413	154.5	8.6	465	1	US-08-752-307B-5	Sequence 5, Appl1	486	150.5	8.3	604	2	US-08-467-602-318	Sequence 318, App
414	154.5	8.6	465	2	US-09-707-802-5	Sequence 5, Appl1	487	150.5	8.3	604	2	US-08-411-295F-244	Sequence 244, App
415	154.5	8.6	465	2	US-09-991-326-5	Sequence 5, Appl1	488	150.5	8.3	610	2	US-08-470-335-236	Sequence 236, App
416	154.5	8.6	602	1	US-08-428-926-5	Sequence 5, Appl1	489	150.5	8.3	610	2	US-08-467-602-332	Sequence 332, App
417	154.5	8.6	602	1	US-08-428-927-5	Sequence 5, Appl1	490	150.5	8.3	610	2	US-08-411-295F-258	Sequence 258, App
418	154.5	8.6	602	1	US-08-428-298-5	Sequence 5, Appl1	491	150.5	8.3	613	2	US-08-470-335-230	Sequence 230, App
419	154.5	8.6	602	1	US-08-339-517-5	Sequence 5, Appl1	492	150.5	8.3	613	2	US-08-467-602-329	Sequence 329, App
420	154.5	8.6	1311	1	US-08-340-011-5	Sequence 5, Appl1	493	150.5	8.3	613	2	US-08-411-295F-255	Sequence 255, App
421	154.5	8.6	1311	2	US-08-901-710-5	Sequence 5, Appl1	494	150.5	8.3	624	2	US-08-467-602-326	Sequence 326, App
422	154.5	8.6	1311	2	US-09-169-079-5	Sequence 5, Appl1	495	150.5	8.3	624	2	US-08-411-295F-252	Sequence 252, App
423	154	8.5	579	2	US-09-173-151A-2	Sequence 2, Appl1	496	150.5	8.3	633	2	US-08-467-602-335	Sequence 335, App
424	154	8.5	686	2	US-09-173-151A-4	Sequence 4, Appl1	497	150.5	8.3	633	2	US-08-411-295F-261	Sequence 261, App
425	153.5	8.5	477	1	US-08-432-016-3	Sequence 3, Appl1	498	150.5	8.3	635	2	US-08-467-602-365	Sequence 365, App
426	153.5	8.5	477	1	US-08-684-594-3	Sequence 3, Appl1	499	150.5	8.3	635	2	US-08-411-295F-291	Sequence 291, App
427	153	8.5	189	2	US-09-270-767-32726	Sequence 32726, A	500	150.5	8.3	638	2	US-08-467-602-360	Sequence 360, App
428	153	8.5	189	2	US-09-270-767-47943	Sequence 47943, A	501	150.5	8.3	638	2	US-08-411-295F-286	Sequence 286, App
429	153	8.5	524	2	US-09-270-767-44009	Sequence 44009, A	502	150.5	8.3	644	2	US-08-467-602-374	Sequence 374, App
430	153	8.5	594	2	US-09-949-016-10605	Sequence 10605, A	503	150.5	8.3	644	2	US-08-411-295F-300	Sequence 300, App
431	152	8.4	351	4	PCT-US93-05703-2	Sequence 2, Appl1	504	150.5	8.3	647	2	US-08-467-602-371	Sequence 371, App
432	152	8.4	1123	2	US-09-949-016-62230	Sequence 6230, Ap	505	150.5	8.3	647	2	US-08-411-295F-297	Sequence 297, App
433	152	8.4	1128	2	US-09-949-016-7532	Sequence 7532, Ap	506	150.5	8.3	658	2	US-08-467-602-368	Sequence 368, App
434	151.5	8.4	227	2	US-09-205-258-947	Sequence 947, App	507	150.5	8.3	658	2	US-08-411-295F-294	Sequence 294, App
435	151.5	8.4	227	2	US-10-004-860-947	Sequence 947, App	508	150.5	8.3	667	2	US-08-467-602-377	Sequence 377, App
436	151.5	8.4	365	2	US-09-949-016-7591	Sequence 7591, Ap	509	150.5	8.3	667	2	US-08-411-295F-303	Sequence 303, App
437	151.5	8.4	422	1	US-08-036-555B-170	Sequence 170, App	510	150.5	8.3	777	1	US-08-874-678-3	Sequence 3, Appl1
438	151.5	8.4	422	1	US-08-469-569-170	Sequence 170, App	511	150.5	8.3	777	1	US-08-643-839-3	Sequence 3, Appl1
439	151.5	8.4	422	1	US-08-428-926-3	Sequence 3, Appl1	512	150.5	8.3	777	2	US-09-348-886-3	Sequence 3, Appl1
440	151.5	8.4	422	1	US-08-249-322A-170	Sequence 170, App	513	150.5	8.3	777	2	US-10-105-901A-3	Sequence 3, Appl1
441	151.5	8.4	422	1	US-08-428-927-3	Sequence 3, Appl1	514	150.5	8.3	818	2	US-08-470-335-234	Sequence 234, App
442	151.5	8.4	422	1	US-08-428-298-3	Sequence 3, Appl1	515	150.5	8.3	818	2	US-08-467-602-321	Sequence 321, App
443	151.5	8.4	422	1	US-08-339-517-3	Sequence 3, Appl1	516	150.5	8.3	818	2	US-08-411-295F-247	Sequence 247, App
444	151.5	8.4	422	1	US-08-469-526A-170	Sequence 170, App	517	150.5	8.3	821	2	US-08-470-335-228	Sequence 228, App
445	151.5	8.4	422	1	US-08-734-591A-170	Sequence 170, App	518	150.5	8.3	821	2	US-08-467-602-319	Sequence 319, App
446	151.5	8.4	422	1	US-08-469-660-170	Sequence 170, App	519	150.5	8.3	821	2	US-08-411-295F-245	Sequence 245, App
447	151.5	8.4	422	2	US-08-341-018-72	Sequence 72, Appl	520	150.5	8.3	827	2	US-08-470-335-237	Sequence 237, App
448	151.5	8.4	422	2	US-08-470-335-170	Sequence 170, App	521	150.5	8.3	827	2	US-08-467-602-333	Sequence 333, App
449	151.5	8.4	422	2	US-08-735-021-170	Sequence 170, App	522	150.5	8.3	827	2	US-08-411-295F-259	Sequence 259, App
450	151.5	8.4	422	2	US-08-734-664A-170	Sequence 170, App	523	150.5	8.3	830	2	US-08-470-335-231	Sequence 330, App
451	151.5	8.4	422	2	US-08-470-339-170	Sequence 170, App	524	150.5	8.3	830	2	US-08-467-602-330	Sequence 330, App
452	151.5	8.4	422	2	US-08-467-602-170	Sequence 170, App	525	150.5	8.3	830	2	US-08-411-295F-256	Sequence 256, App
453	151.5	8.4	422	2	US-08-411-295F-65	Sequence 65, Appl	526	150.5	8.3	841	2	US-08-467-602-327	Sequence 327, App
454	151.5	8.4	422	2	US-08-411-295F-66	Sequence 66, Appl	527	150.5	8.3	841	2	US-08-411-295F-253	Sequence 253, App
455	151.5	8.4	422	2	US-08-411-295F-69	Sequence 69, Appl	528	150.5	8.3	850	2	US-08-467-602-336	Sequence 336, App
456	151.5	8.4	422	2	US-08-411-295F-103	Sequence 103, App	529	150.5	8.3	850	2	US-08-411-295F-262	Sequence 262, App
457	151.5	8.4	422	4	PCT-US94-05083C-166	Sequence 166, App	530	150.5	8.3	852	2	US-08-467-602-363	Sequence 363, App
458	151.5	8.4	422	4	PCT-US94-05083C-185	Sequence 185, App	531	150.5	8.3	852	2	US-08-411-295F-289	Sequence 289, App
459	151.5	8.4	422	4	PCT-US95-06848A-170	Sequence 170, App	532	150.5	8.3	855	2	US-08-467-602-361	Sequence 361, App
460	151.5	8.4	1363	1	US-08-874-678-32	Sequence 32, Appl	533	150.5	8.3	855	2	US-08-411-295F-287	Sequence 287, App
461	151.5	8.4	1363	2	US-08-643-839-32	Sequence 32, Appl	534	150.5	8.3	861	2	US-08-467-602-375	Sequence 375, App
462	151.5	8.4	1363	2	US-09-348-886-32	Sequence 32, Appl	535	150.5	8.3	861	2	US-08-411-295F-301	Sequence 301, App
463	151.5	8.4	1363	2	US-10-105-901A-32	Sequence 32, Appl	536	150.5	8.3	864	2	US-08-467-602-372	Sequence 372, App
464	151	8.4	874	1	US-08-456-647B-6	Sequence 6, Appl1	537	150.5	8.3	864	2	US-08-411-295F-298	Sequence 298, App
465	151	8.4	874	1	US-08-237-401A-6	Sequence 6, Appl1	538	150.5	8.3	865	2	US-08-470-335-235	Sequence 235, App

539	150.5	8.3	865	2	US-08-467-602-322	Sequence 322, App	612	143.5	7.9	662	1	US-08-261-304-7	Sequence 7, Appli
540	150.5	8.3	865	2	US-08-411-295F-248	Sequence 248, App	613	143	7.9	661	1	US-08-232-538-12	Sequence 12, Appl
541	150.5	8.3	868	2	US-08-470-335-229	Sequence 229, App	614	143	7.9	661	1	US-08-786-164-12	Sequence 12, Appl
542	150.5	8.3	868	2	US-08-467-602-317	Sequence 317, App	615	143	7.9	687	1	US-08-232-538-6	Sequence 6, Appli
543	150.5	8.3	868	2	US-08-411-295F-243	Sequence 243, App	616	143	7.9	687	1	US-08-786-164-6	Sequence 6, Appli
544	150.5	8.3	874	2	US-08-470-335-238	Sequence 238, App	617	143	7.9	687	2	US-09-427-353-2	Sequence 2, Appli
545	150.5	8.3	874	2	US-08-467-602-334	Sequence 334, App	618	142.5	7.9	263	2	US-08-411-295F-77	Sequence 77, Appl
546	150.5	8.3	874	2	US-08-411-295F-260	Sequence 260, App	619	142.5	7.9	431	2	US-09-592-998C-9	Sequence 9, Appli
547	150.5	8.3	875	2	US-08-467-602-369	Sequence 369, App	620	142.5	7.9	435	2	US-09-592-998C-10	Sequence 10, Appl
548	150.5	8.3	875	2	US-08-411-295F-295	Sequence 295, App	621	142.5	7.9	735	4	PCT-US93-00031-13	Sequence 13, Appl
549	150.5	8.3	877	2	US-08-470-335-232	Sequence 232, App	622	142.5	7.9	739	2	US-08-482-073-6	Sequence 6, Appli
550	150.5	8.3	877	2	US-08-467-602-331	Sequence 331, App	623	142.5	7.9	739	4	PCT-US93-00031-9	Sequence 9, Appli
551	150.5	8.3	877	2	US-08-411-295F-257	Sequence 257, App	624	141.5	7.8	254	2	US-08-470-335-193	Sequence 193, App
552	150.5	8.3	884	2	US-08-467-602-378	Sequence 378, App	625	141.5	7.8	257	2	US-08-470-335-192	Sequence 6, Appli
553	150.5	8.3	884	2	US-08-411-295F-304	Sequence 304, App	626	141.5	7.8	257	2	US-08-470-339-193	Sequence 193, App
554	150.5	8.3	888	2	US-08-467-602-325	Sequence 325, App	627	141.5	7.8	257	2	US-08-467-602-387	Sequence 387, App
555	150.5	8.3	888	2	US-08-411-295F-251	Sequence 251, App	628	141.5	7.8	257	2	US-08-411-295F-6	Sequence 6, Appli
556	150.5	8.3	897	2	US-08-467-602-337	Sequence 337, App	629	141.5	7.8	283	2	US-08-411-295F-4	Sequence 4, Appli
557	150.5	8.3	897	2	US-08-411-295F-263	Sequence 263, App	630	141.5	7.8	280	2	US-08-341-018-56	Sequence 56, Appl
558	150.5	8.3	899	2	US-08-467-602-364	Sequence 364, App	631	141.5	7.8	280	2	US-08-470-335-192	Sequence 192, App
559	150.5	8.3	899	2	US-08-411-295F-290	Sequence 290, App	632	141.5	7.8	280	2	US-08-470-339-192	Sequence 192, App
560	150.5	8.3	902	2	US-08-467-602-359	Sequence 359, App	633	141.5	7.8	280	2	US-08-467-602-386	Sequence 386, App
561	150.5	8.3	902	2	US-08-411-295F-285	Sequence 285, App	634	141.5	7.8	280	2	US-08-411-295F-49	Sequence 49, Appl
562	150.5	8.3	908	2	US-08-467-602-376	Sequence 376, App	635	141.5	7.8	280	2	US-08-411-295F-95	Sequence 95, Appl
563	150.5	8.3	908	2	US-08-411-295F-302	Sequence 302, App	636	141.5	7.8	388	1	US-08-445-640-12	Sequence 12, Appl
564	150.5	8.3	911	2	US-08-467-602-373	Sequence 373, App	637	141.5	7.8	388	2	US-08-170-558-12	Sequence 12, Appl
565	150.5	8.3	911	2	US-08-411-295F-299	Sequence 299, App	638	141.5	7.8	388	2	US-08-447-314-12	Sequence 12, Appl
566	150.5	8.3	922	2	US-08-467-602-367	Sequence 367, App	639	141.5	7.8	388	2	US-08-445-461-12	Sequence 12, Appl
567	150.5	8.3	922	2	US-08-411-295F-293	Sequence 293, App	640	141.5	7.8	388	2	US-09-223-490-12	Sequence 12, Appl
568	150.5	8.3	931	2	US-08-467-602-379	Sequence 379, App	641	141.5	7.8	985	2	US-09-999-833A-211	Sequence 211, App
569	150.5	8.3	931	2	US-08-411-295F-305	Sequence 305, App	642	141.5	7.8	985	2	US-10-020-445A-211	Sequence 211, App
570	150.5	8.3	1298	1	US-08-322-616-33	Sequence 33, Appl	643	141	7.8	471	2	US-09-949-016-9042	Sequence 9042, Ap
571	150.5	8.3	1298	1	US-08-340-011-2	Sequence 2, Appli	644	141	7.8	471	2	US-09-949-016-9043	Sequence 9043, Ap
572	150.5	8.3	1298	2	US-08-901-710-2	Sequence 2, Appli	645	141	7.8	471	2	US-09-949-016-9044	Sequence 9044, Ap
573	150.5	8.3	1298	2	US-08-446-648-33	Sequence 33, Appl	646	141	7.8	471	2	US-09-949-016-9045	Sequence 9045, Ap
574	150.5	8.3	1298	2	US-09-982-610-33	Sequence 33, Appl	647	141	7.8	471	2	US-09-949-016-9046	Sequence 9046, Ap
575	150.5	8.3	1298	2	US-09-169-079-2	Sequence 2, Appli	648	141	7.8	471	2	US-09-949-016-9048	Sequence 9048, Ap
576	150.5	8.3	1298	4	PCT-US95-04228-33	Sequence 33, Appl	649	141	7.8	471	2	US-09-949-016-9048	Sequence 9048, Ap
577	150.5	8.3	1362	1	US-08-874-678-33	Sequence 33, Appl	650	141	7.8	471	2	US-09-949-016-9049	Sequence 9049, Ap
578	150.5	8.3	1362	2	US-08-643-839-33	Sequence 33, Appl	651	141	7.8	471	2	US-09-949-016-9050	Sequence 9050, Ap
579	150.5	8.3	1362	2	US-09-348-886-33	Sequence 33, Appl	652	141	7.8	471	2	US-09-949-016-9051	Sequence 9051, Ap
580	150.5	8.3	1362	2	US-10-105-901A-33	Sequence 33, Appl	653	141	7.8	821	1	US-08-451-822A-13	Sequence 13, Appl
581	150.5	8.3	1363	1	US-08-340-011-4	Sequence 4, Appli	654	141	7.8	821	2	US-08-323-430-13	Sequence 13, Appl
582	150.5	8.3	1363	2	US-08-901-710-4	Sequence 4, Appli	655	140.5	7.8	257	2	US-08-411-295F-78	Sequence 78, Appl
583	150.5	8.3	1363	2	US-09-375-248-2	Sequence 2, Appli	656	140.5	7.8	552	2	US-09-969-532-8	Sequence 8, Appli
584	150.5	8.3	1363	2	US-09-169-079-4	Sequence 4, Appli	657	140.5	7.8	553	2	US-09-969-532-6	Sequence 6, Appli
585	150.5	8.3	1368	1	US-08-874-678-34	Sequence 34, Appl	658	140.5	7.8	566	2	US-09-969-532-4	Sequence 4, Appli
586	150.5	8.3	1368	2	US-08-643-839-34	Sequence 34, Appl	659	140.5	7.8	577	2	US-09-969-532-2	Sequence 2, Appli
587	150.5	8.3	1368	2	US-09-348-886-34	Sequence 34, Appl	660	140.5	7.8	577	2	US-09-969-532-10	Sequence 10, Appl
588	150.5	8.3	1368	2	US-10-105-901A-34	Sequence 34, Appl	661	140.5	7.8	589	2	US-09-866-510-12	Sequence 12, Appl
589	150	8.3	335	1	US-08-471-570-14	Sequence 14, Appl	662	140.5	7.8	762	2	US-09-949-016-7568	Sequence 7568, Ap
590	150	8.3	643	1	US-08-471-570-6	Sequence 6, Appli	663	140.5	7.8	886	2	US-09-969-532-16	Sequence 16, Appl
591	150	8.3	769	1	US-08-471-570-8	Sequence 8, Appli	664	140.5	7.8	897	2	US-09-969-532-14	Sequence 14, Appl
592	149.5	8.3	1501	1	US-08-447-464-3	Sequence 3, Appli	665	140.5	7.8	900	2	US-09-969-532-12	Sequence 12, Appl
593	149.5	8.3	1501	1	US-08-716-679-3	Sequence 3, Appli	666	140.5	7.8	911	2	US-09-969-532-10	Sequence 10, Appl
594	149	8.3	388	1	US-08-429-742-4	Sequence 4, Appli	667	140.5	7.8	1088	2	US-09-861-403-4	Sequence 4, Appli
595	148.5	8.2	1911	1	US-08-348-006B-5	Sequence 5, Appli	668	140.5	7.8	1089	1	US-08-180-195-36	Sequence 36, Appl
596	148.5	8.2	1911	1	US-08-800-825A-5	Sequence 5, Appli	669	140.5	7.8	1089	1	US-08-168-917-4	Sequence 4, Appli
597	148.5	8.2	1911	2	US-09-158-657-5	Sequence 5, Appli	670	140.5	7.8	1089	1	US-08-477-329-36	Sequence 36, Appl
598	148.5	8.2	1911	4	PCT-US94-10166-5	Sequence 5, Appli	671	140.5	7.8	1089	1	US-08-458-458-36	Sequence 36, Appl
599	148	8.2	602	1	US-08-168-091A-2	Sequence 2, Appli	672	140.5	7.8	1089	1	US-08-460-490-4	Sequence 4, Appli
600	148	8.2	820	1	US-08-166-717D-6	Sequence 6, Appli	673	140.5	7.8	1089	2	US-08-980-400-36	Sequence 36, Appl
601	147.5	8.2	403	2	US-09-638-649-5	Sequence 5, Appli	674	140.5	7.8	1089	2	US-08-462-728-2	Sequence 2, Appli
602	147.5	8.2	403	2	US-09-638-648-5	Sequence 5, Appli	675	140.5	7.8	1089	2	US-09-583-459A-36	Sequence 36, Appl
603	145.5	8.1	252	2	US-09-270-767-44627	Sequence 44627, A	676	140.5	7.8	1089	2	US-09-583-210-36	Sequence 36, Appl
604	145.5	8.1	549	2	US-09-858-664A-5	Sequence 5, Appli	677	140.5	7.8	1089	2	US-09-583-449A-36	Sequence 36, Appl
605	145.5	8.1	549	2	US-10-274-978-6	Sequence 6, Appli	678	140.5	7.8	1089	2	US-09-435-059-36	Sequence 36, Appl
606	145.5	8.1	549	2	US-10-697-263-6	Sequence 6, Appli	679	140.5	7.8	1089	2	US-08-461-917-2	Sequence 2, Appli
607	145	8.0	972	2	US-08-750-141A-2	Sequence 2, Appli	680	140.5	7.8	1089	2	US-08-464-436-2	Sequence 2, Appli
608	145	8.0	972	2	US-09-944-807-10	Sequence 10, Appl	681	140.5	7.8	1089	2	US-08-464-436-2	Sequence 2, Appli
609	144	8.0	891	2	US-09-345-473E-25	Sequence 25, Appl	682	140.5	7.8	1089	2	US-09-769-987-2	Sequence 2, Appli
610	144	8.0	891	2	US-09-862-027-25	Sequence 25, Appl	683	140.5	7.8	1089	2	US-09-866-510-2	Sequence 2, Appli
611	143.5	7.9	344	1	US-08-602-725-34	Sequence 34, Appl	684	140.5	7.8	1089	2	US-09-866-510-4	Sequence 4, Appli

685	140.5	7.6	1089	2	US-09-866-510-6	Sequence 6, Appli	758	138.5	7.7	601	2	US-08-411-295F-178	Sequence 178, App
686	140.5	7.8	1089	2	US-09-866-510-8	Sequence 8, Appli	759	138.5	7.7	603	2	US-08-467-602-279	Sequence 279, App
687	140.5	7.8	1089	2	US-09-866-510-10	Sequence 10, Appl	760	138.5	7.7	606	2	US-08-411-295F-205	Sequence 205, App
688	140.5	7.8	1089	2	US-09-919-497-90	Sequence 90, Appl	761	138.5	7.7	603	2	US-08-467-602-277	Sequence 277, App
689	140.5	7.8	1089	4	US-09-949-016-6703	Sequence 6703, Ap	762	138.5	7.7	606	2	US-08-411-295F-203	Sequence 203, App
690	140.5	7.8	1089	4	PCT-US92-00730-4	Sequence 4, Appli	763	138.5	7.7	612	2	US-08-467-602-291	Sequence 291, App
691	140.5	7.8	1089	4	PCT-US92-00862-4	Sequence 4, Appli	764	138.5	7.7	612	2	US-08-411-295F-217	Sequence 217, App
692	140	7.8	203	2	US-09-270-767-60345	Sequence 60345, A	765	138.5	7.7	615	2	US-08-467-602-288	Sequence 288, App
693	140	7.8	801	2	US-09-383-630-6	Sequence 6, Appli	766	138.5	7.7	615	2	US-08-411-295F-214	Sequence 214, App
694	140	7.8	890	1	US-08-445-640-2	Sequence 2, Appli	767	138.5	7.7	616	2	US-08-467-602-238	Sequence 238, App
695	140	7.8	890	2	US-08-170-558-2	Sequence 2, Appli	768	138.5	7.7	616	2	US-08-411-295F-164	Sequence 164, App
696	140	7.8	890	2	US-08-447-314-2	Sequence 2, Appli	769	138.5	7.7	619	2	US-08-467-602-233	Sequence 233, App
697	140	7.8	890	2	US-08-445-461-2	Sequence 2, Appli	770	138.5	7.7	619	2	US-08-411-295F-159	Sequence 159, App
698	140	7.8	890	2	US-09-223-490-2	Sequence 2, Appli	771	138.5	7.7	625	2	US-08-467-602-250	Sequence 250, App
699	140	7.8	911	1	US-08-286-305A-1	Sequence 1, Appli	772	138.5	7.7	625	2	US-08-411-295F-176	Sequence 176, App
700	140	7.8	911	1	US-08-441-104A-1	Sequence 1, Appli	773	138.5	7.7	626	2	US-08-467-602-285	Sequence 285, App
701	140	7.8	911	1	US-08-440-816A-1	Sequence 1, Appli	774	138.5	7.7	626	2	US-08-411-295F-211	Sequence 211, App
702	140	7.8	911	2	US-09-417-381A-1	Sequence 1, Appli	775	138.5	7.7	628	2	US-08-467-602-247	Sequence 247, App
703	140	7.8	976	2	US-08-750-141A-1	Sequence 1, Appli	776	138.5	7.7	628	2	US-08-411-295F-173	Sequence 173, App
704	139.5	7.7	263	2	US-08-341-018-4	Sequence 4, Appli	777	138.5	7.7	635	2	US-08-467-602-284	Sequence 284, App
705	139.5	7.7	263	2	US-08-470-335-191	Sequence 191, App	778	138.5	7.7	635	2	US-08-411-295F-220	Sequence 220, App
706	139.5	7.7	263	2	US-08-470-339-191	Sequence 191, App	779	138.5	7.7	639	2	US-08-467-602-241	Sequence 241, App
707	139.5	7.7	263	2	US-08-467-602-385	Sequence 385, App	780	138.5	7.7	639	2	US-08-411-295F-167	Sequence 167, App
708	139.5	7.7	419	6	5169835-2	Patent No. 5169835	781	138.5	7.7	648	2	US-08-467-602-253	Sequence 253, App
709	139	7.7	212	1	US-08-282-951-6	Sequence 6, Appli	782	138.5	7.7	648	2	US-08-411-295F-179	Sequence 179, App
710	138.5	7.7	140	2	US-08-986-485-4	Sequence 4, Appli	783	138.5	7.7	650	2	US-08-467-602-280	Sequence 280, App
711	138.5	7.7	173	2	US-08-467-602-240	Sequence 240, App	784	138.5	7.7	650	2	US-08-411-295F-206	Sequence 206, App
712	138.5	7.7	173	2	US-08-411-295F-166	Sequence 166, App	785	138.5	7.7	653	2	US-08-467-602-275	Sequence 275, App
713	138.5	7.7	176	2	US-08-467-602-236	Sequence 236, App	786	138.5	7.7	653	2	US-08-411-295F-201	Sequence 201, App
714	138.5	7.7	176	2	US-08-411-295F-162	Sequence 162, App	787	138.5	7.7	659	2	US-08-467-602-292	Sequence 292, App
715	138.5	7.7	196	2	US-08-467-602-244	Sequence 244, App	788	138.5	7.7	659	2	US-08-411-295F-218	Sequence 218, App
716	138.5	7.7	196	2	US-08-411-295F-170	Sequence 170, App	789	138.5	7.7	662	2	US-08-467-602-289	Sequence 289, App
717	138.5	7.7	207	2	US-08-467-602-282	Sequence 282, App	790	138.5	7.7	662	2	US-08-411-295F-215	Sequence 215, App
718	138.5	7.7	207	2	US-08-411-295F-208	Sequence 208, App	791	138.5	7.7	673	2	US-08-467-602-283	Sequence 283, App
719	138.5	7.7	210	2	US-08-467-602-278	Sequence 278, App	792	138.5	7.7	673	2	US-08-411-295F-209	Sequence 209, App
720	138.5	7.7	210	2	US-08-411-295F-204	Sequence 204, App	793	138.5	7.7	682	2	US-08-467-602-295	Sequence 295, App
721	138.5	7.7	230	2	US-08-467-602-286	Sequence 286, App	794	138.5	7.7	682	2	US-08-411-295F-221	Sequence 221, App
722	138.5	7.7	230	2	US-08-411-295F-212	Sequence 212, App	795	137	7.6	514	2	US-09-949-016-11380	Sequence 11380, A
723	138.5	7.7	352	2	US-08-467-602-239	Sequence 239, App	796	137	7.6	517	2	US-09-723-368-4	Sequence 4, Appli
724	138.5	7.7	352	2	US-08-411-295F-165	Sequence 165, App	797	136.5	7.6	388	1	US-08-445-640-6	Sequence 6, Appli
725	138.5	7.7	355	2	US-08-467-602-234	Sequence 234, App	798	136.5	7.6	388	2	US-08-170-558-6	Sequence 6, Appli
726	138.5	7.7	355	2	US-08-411-295F-160	Sequence 160, App	799	136.5	7.6	388	2	US-08-447-314-6	Sequence 6, Appli
727	138.5	7.7	361	2	US-08-467-602-248	Sequence 248, App	800	136.5	7.6	388	2	US-08-445-461-6	Sequence 6, Appli
728	138.5	7.7	361	2	US-08-411-295F-174	Sequence 174, App	801	136.5	7.6	388	2	US-09-223-490-6	Sequence 6, Appli
729	138.5	7.7	364	2	US-08-467-602-245	Sequence 245, App	802	136.5	7.6	498	2	US-09-354-151-2	Sequence 2, Appli
730	138.5	7.7	364	2	US-08-411-295F-171	Sequence 171, App	803	136.5	7.6	738	2	US-08-478-208-32	Sequence 32, Appl
731	138.5	7.7	375	2	US-08-467-602-242	Sequence 242, App	804	136.5	7.6	738	2	US-09-336-536-73	Sequence 73, Appl
732	138.5	7.7	375	2	US-08-411-295F-168	Sequence 168, App	805	136.5	7.6	738	6	5264554-2	Patent No. 5264554
733	138.5	7.7	384	2	US-08-467-602-251	Sequence 251, App	806	136	7.5	393	1	US-08-429-742-2	Sequence 2, Appli
734	138.5	7.7	384	2	US-08-411-295F-177	Sequence 177, App	807	136	7.5	458	2	US-09-435-958A-1	Sequence 1, Appli
735	138.5	7.7	386	2	US-08-467-602-281	Sequence 281, App	808	136	7.5	644	4	PCT-US93-00031-21	Sequence 21, Appl
736	138.5	7.7	386	2	US-08-411-295F-207	Sequence 207, App	809	135.5	7.5	371	2	US-08-411-295F-308	Sequence 308, App
737	138.5	7.7	389	2	US-08-467-602-276	Sequence 276, App	810	135.5	7.5	405	2	US-08-467-602-384	Sequence 384, App
738	138.5	7.7	389	2	US-08-411-295F-202	Sequence 202, App	811	135.5	7.5	405	2	US-08-411-295F-307	Sequence 307, App
739	138.5	7.7	395	2	US-08-467-602-290	Sequence 290, App	812	135.5	7.5	501	2	US-08-891-845-10	Sequence 10, Appl
740	138.5	7.7	395	2	US-08-411-295F-216	Sequence 216, App	813	135.5	7.5	501	2	US-09-514-573-10	Sequence 10, Appl
741	138.5	7.7	398	2	US-08-467-602-287	Sequence 287, App	814	135.5	7.5	501	2	US-10-290-578-10	Sequence 10, Appl
742	138.5	7.7	398	2	US-08-411-295F-213	Sequence 213, App	815	135.5	7.5	768	2	US-08-891-845-2	Sequence 2, Appli
743	138.5	7.7	409	2	US-08-467-602-284	Sequence 284, App	816	135.5	7.5	768	2	US-09-514-573-2	Sequence 2, Appli
744	138.5	7.7	409	2	US-08-411-295F-210	Sequence 210, App	817	135.5	7.5	768	2	US-10-290-578-2	Sequence 2, Appli
745	138.5	7.7	418	2	US-08-467-602-293	Sequence 293, App	818	135	7.5	492	2	US-08-462-794-11	Sequence 11, Appl
746	138.5	7.7	418	2	US-08-411-295F-219	Sequence 219, App	819	135	7.5	497	2	US-09-499-846-6	Sequence 6, Appli
747	138.5	7.7	569	2	US-08-467-602-237	Sequence 237, App	820	135	7.5	497	2	US-09-499-846-10	Sequence 10, Appl
748	138.5	7.7	569	2	US-08-411-295F-163	Sequence 163, App	821	135	7.5	525	2	US-09-499-846-4	Sequence 4, Appli
749	138.5	7.7	572	2	US-08-467-602-235	Sequence 235, App	822	135	7.5	525	2	US-09-499-846-8	Sequence 8, Appli
750	138.5	7.7	572	2	US-08-411-295F-161	Sequence 161, App	823	134.5	7.4	349	2	US-08-470-335-188	Sequence 188, App
751	138.5	7.7	578	2	US-08-467-602-249	Sequence 249, App	824	134.5	7.4	382	2	US-08-467-602-382	Sequence 382, App
752	138.5	7.7	578	2	US-08-411-295F-175	Sequence 175, App	825	134.5	7.4	434	2	US-09-540-245A-19	Sequence 19, Appl
753	138.5	7.7	581	2	US-08-467-602-246	Sequence 246, App	826	134.5	7.4	434	2	US-10-289-776-19	Sequence 19, Appl
754	138.5	7.7	581	2	US-08-411-295F-172	Sequence 172, App	827	134.5	7.4	456	2	US-08-470-335-246	Sequence 246, App
755	138.5	7.7	592	2	US-08-467-602-243	Sequence 243, App	828	134.5	7.4	456	2	US-08-467-602-303	Sequence 303, App
756	138.5	7.7	592	2	US-08-411-295F-169	Sequence 169, App	829	134.5	7.4	456	2	US-08-411-295F-229	Sequence 229, App
757	138.5	7.7	601	2	US-08-467-602-252	Sequence 252, App	830	134.5	7.4	459	2	US-08-470-335-239	Sequence 239, App

831	134.5	7.4	459	2	US-08-467-602-299	Sequence 299, App	904	134.5	7.4	899	2	US-08-470-335-249	Sequence 249, App
832	134.5	7.4	459	2	US-08-411-295F-225	Sequence 225, App	905	134.5	7.4	899	2	US-08-467-602-301	Sequence 301, App
833	134.5	7.4	479	2	US-08-467-602-307	Sequence 307, App	906	134.5	7.4	899	2	US-08-411-295F-227	Sequence 227, App
834	134.5	7.4	479	2	US-08-411-295F-233	Sequence 233, App	907	134.5	7.4	902	2	US-08-470-335-242	Sequence 242, App
835	134.5	7.4	490	2	US-08-467-602-345	Sequence 345, App	908	134.5	7.4	902	2	US-08-467-602-296	Sequence 296, App
836	134.5	7.4	490	2	US-08-411-295F-271	Sequence 271, App	909	134.5	7.4	902	2	US-08-411-295F-222	Sequence 222, App
837	134.5	7.4	493	2	US-08-467-602-341	Sequence 341, App	910	134.5	7.4	908	2	US-08-470-335-252	Sequence 252, App
838	134.5	7.4	493	2	US-08-411-295F-267	Sequence 267, App	911	134.5	7.4	908	2	US-08-467-602-313	Sequence 313, App
839	134.5	7.4	513	2	US-08-467-602-349	Sequence 349, App	912	134.5	7.4	908	2	US-08-411-295F-239	Sequence 239, App
840	134.5	7.4	513	2	US-08-411-295F-275	Sequence 275, App	913	134.5	7.4	909	2	US-08-467-602-348	Sequence 348, App
841	134.5	7.4	526	1	US-08-471-570-4	Sequence 4, Appl	914	134.5	7.4	909	2	US-08-411-295F-274	Sequence 274, App
842	134.5	7.4	534	2	US-09-651-200-6	Sequence 6, Appl	915	134.5	7.4	911	2	US-08-470-335-245	Sequence 245, App
843	134.5	7.4	534	2	US-09-651-200-24	Sequence 24, Appl	916	134.5	7.4	911	2	US-08-467-602-310	Sequence 310, App
844	134.5	7.4	635	2	US-08-470-335-247	Sequence 247, App	917	134.5	7.4	911	2	US-08-411-295F-236	Sequence 236, App
845	134.5	7.4	635	2	US-08-467-602-302	Sequence 302, App	918	134.5	7.4	918	2	US-08-467-602-357	Sequence 357, App
846	134.5	7.4	635	2	US-08-411-295F-228	Sequence 228, App	919	134.5	7.4	918	2	US-08-411-295F-283	Sequence 283, App
847	134.5	7.4	638	2	US-08-470-335-240	Sequence 240, App	920	134.5	7.4	922	2	US-08-467-602-304	Sequence 304, App
848	134.5	7.4	638	2	US-08-467-602-297	Sequence 297, App	921	134.5	7.4	922	2	US-08-411-295F-230	Sequence 230, App
849	134.5	7.4	638	2	US-08-411-295F-223	Sequence 223, App	922	134.5	7.4	931	2	US-08-467-602-316	Sequence 316, App
850	134.5	7.4	643	4	PCT-US93-00031-19	Sequence 19, Appl	923	134.5	7.4	931	2	US-08-411-295F-242	Sequence 242, App
851	134.5	7.4	644	2	US-08-470-335-250	Sequence 250, App	924	134.5	7.4	933	2	US-08-467-602-343	Sequence 343, App
852	134.5	7.4	644	2	US-08-467-602-311	Sequence 311, App	925	134.5	7.4	933	2	US-08-411-295F-269	Sequence 269, App
853	134.5	7.4	644	2	US-08-411-295F-237	Sequence 237, App	926	134.5	7.4	936	2	US-08-467-602-338	Sequence 338, App
854	134.5	7.4	647	2	US-08-470-335-243	Sequence 243, App	927	134.5	7.4	936	2	US-08-411-295F-264	Sequence 264, App
855	134.5	7.4	647	2	US-09-009-490A-91	Sequence 91, Appl	928	134.5	7.4	942	2	US-08-467-602-355	Sequence 355, App
856	134.5	7.4	647	2	US-08-482-073-5	Sequence 5, Appl	929	134.5	7.4	942	2	US-08-411-295F-281	Sequence 281, App
857	134.5	7.4	647	2	US-08-467-602-308	Sequence 308, App	930	134.5	7.4	945	2	US-08-467-602-352	Sequence 352, App
858	134.5	7.4	647	2	US-08-411-295F-234	Sequence 234, App	931	134.5	7.4	945	2	US-08-411-295F-278	Sequence 278, App
859	134.5	7.4	647	2	US-09-982-262C-92	Sequence 92, Appl	932	134.5	7.4	956	2	US-08-467-602-346	Sequence 346, App
860	134.5	7.4	647	4	PCT-US93-00031-11	Sequence 11, Appl	933	134.5	7.4	956	2	US-08-411-295F-272	Sequence 272, App
861	134.5	7.4	647	4	PCT-US93-00031-23	Sequence 23, Appl	934	134.5	7.4	965	2	US-08-467-602-358	Sequence 358, App
862	134.5	7.4	652	1	US-08-471-570-10	Sequence 10, Appl	935	134.5	7.4	965	2	US-08-411-295F-284	Sequence 284, App
863	134.5	7.4	658	2	US-08-467-602-305	Sequence 305, App	936	134	7.4	424	6	5169835-6	Patent No. 5169835
864	134.5	7.4	658	2	US-08-411-295F-231	Sequence 31, App	937	133.5	7.4	488	2	US-09-499-846-12	Sequence 12, Appl
865	134.5	7.4	667	2	US-08-467-602-314	Sequence 231, App	938	133.5	7.4	888	1	US-08-445-640-35	Sequence 35, Appl
866	134.5	7.4	667	2	US-08-411-295F-240	Sequence 240, App	939	133.5	7.4	888	2	US-08-170-558-35	Sequence 35, Appl
867	134.5	7.4	669	2	US-08-467-602-344	Sequence 344, App	940	133.5	7.4	888	2	US-08-447-314-35	Sequence 35, Appl
868	134.5	7.4	669	2	US-08-411-295F-270	Sequence 270, App	941	133.5	7.4	888	2	US-08-445-461-35	Sequence 35, Appl
869	134.5	7.4	672	2	US-08-467-602-339	Sequence 339, App	942	133.5	7.4	888	2	US-09-223-490-35	Sequence 35, Appl
870	134.5	7.4	672	2	US-08-411-295F-265	Sequence 265, App	943	133	7.4	317	2	US-09-684-708A-23	Sequence 23, Appl
871	134.5	7.4	678	2	US-08-467-602-353	Sequence 353, App	944	133	7.4	322	2	US-09-383-586-33	Sequence 33, Appl
872	134.5	7.4	678	2	US-08-411-295F-279	Sequence 279, App	945	133	7.4	322	2	US-09-823-038A-33	Sequence 33, Appl
873	134.5	7.4	681	2	US-08-467-602-350	Sequence 350, App	946	133	7.4	323	2	US-09-684-708A-25	Sequence 25, Appl
874	134.5	7.4	681	2	US-08-411-295F-276	Sequence 276, App	947	133	7.4	612	1	US-08-359-705B-8	Sequence 8, Appl
875	134.5	7.4	692	2	US-08-467-602-347	Sequence 347, App	948	133	7.4	612	1	US-08-286-846A-8	Sequence 8, Appl
876	134.5	7.4	692	2	US-08-411-295F-273	Sequence 273, App	949	133	7.4	612	1	US-08-457-880A-8	Sequence 8, Appl
877	134.5	7.4	701	2	US-08-467-602-356	Sequence 356, App	950	133	7.4	612	2	US-08-444-622A-8	Sequence 8, Appl
878	134.5	7.4	701	2	US-08-411-295F-282	Sequence 282, App	951	133	7.4	612	2	US-08-942-562-8	Sequence 8, Appl
879	134.5	7.4	740	4	PCT-US93-00031-17	Sequence 17, Appl	952	133	7.4	612	2	US-09-156-923-8	Sequence 8, Appl
880	134.5	7.4	852	2	US-08-470-335-248	Sequence 248, App	953	133	7.4	816	2	US-09-949-016-10904	Sequence 10904, A
881	134.5	7.4	852	2	US-08-467-602-300	Sequence 300, App	954	133	7.4	839	1	US-08-359-705B-6	Sequence 6, Appl
882	134.5	7.4	852	2	US-08-411-295F-226	Sequence 226, App	955	133	7.4	839	1	US-08-286-846A-6	Sequence 6, Appl
883	134.5	7.4	855	2	US-08-470-335-241	Sequence 241, App	956	133	7.4	839	1	US-08-457-880A-6	Sequence 6, Appl
884	134.5	7.4	855	2	US-08-467-602-298	Sequence 298, App	957	133	7.4	839	2	US-08-444-622A-6	Sequence 6, Appl
885	134.5	7.4	855	2	US-08-411-295F-224	Sequence 224, App	958	133	7.4	839	2	US-08-942-562-6	Sequence 6, Appl
886	134.5	7.4	861	2	US-08-470-335-251	Sequence 251, App	959	133	7.4	839	2	US-09-156-923-6	Sequence 6, Appl
887	134.5	7.4	861	2	US-08-467-602-312	Sequence 312, App	960	133	7.4	850	1	US-08-286-305A-7	Sequence 7, Appl
888	134.5	7.4	861	2	US-08-411-295F-238	Sequence 238, App	961	133	7.4	850	1	US-08-441-104A-7	Sequence 7, Appl
889	134.5	7.4	864	2	US-08-470-335-244	Sequence 244, App	962	133	7.4	850	1	US-08-440-816A-7	Sequence 7, Appl
890	134.5	7.4	864	2	US-08-467-602-309	Sequence 309, App	963	133	7.4	850	2	US-09-417-381A-7	Sequence 7, Appl
891	134.5	7.4	864	2	US-08-411-295F-235	Sequence 235, App	964	132	7.3	387	2	US-09-175-928-2	Sequence 2, Appl
892	134.5	7.4	875	2	US-08-467-602-306	Sequence 306, App	965	132	7.3	408	2	US-09-724-864-62	Sequence 62, Appl
893	134.5	7.4	875	2	US-08-411-295F-232	Sequence 232, App	966	131.5	7.3	312	2	US-09-254-465A-9	Sequence 9, Appl
894	134.5	7.4	884	2	US-08-467-602-315	Sequence 315, App	967	131.5	7.3	312	2	US-09-507-794A-64	Sequence 64, Appl
895	134.5	7.4	884	2	US-08-411-295F-241	Sequence 241, App	968	131.5	7.3	312	2	US-09-905-125A-64	Sequence 64, Appl
896	134.5	7.4	886	2	US-08-467-602-342	Sequence 342, App	969	131.5	7.3	312	2	US-09-902-775A-64	Sequence 64, Appl
897	134.5	7.4	886	2	US-08-411-295F-268	Sequence 268, App	970	131.5	7.3	312	2	US-09-906-700-64	Sequence 64, Appl
898	134.5	7.4	889	2	US-08-467-602-340	Sequence 340, App	971	131.5	7.3	312	2	US-09-903-603A-64	Sequence 64, Appl
899	134.5	7.4	889	2	US-08-411-295F-266	Sequence 266, App	972	131.5	7.3	312	2	US-09-904-920A-64	Sequence 64, Appl
900	134.5	7.4	895	2	US-08-467-602-354	Sequence 354, App	973	131.5	7.3	312	2	US-09-909-064-64	Sequence 64, Appl
901	134.5	7.4	895	2	US-08-411-295F-280	Sequence 280, App	974	131.5	7.3	312	2	US-09-905-381A-64	Sequence 64, Appl
902	134.5	7.4	898	2	US-08-467-602-351	Sequence 351, App	975	131.5	7.3	312	2	US-09-906-618-64	Sequence 64, Appl
903	134.5	7.4	898	2	US-08-411-295F-277	Sequence 277, App	976	131.5	7.3	312	2	US-09-953-499-9	Sequence 9, Appl

977	131.5	7.3	312	2	US-09-906-646-64	Sequence 64, Appl	1050	127.5	7.1	241	2	US-08-411-295F-94	Sequence 94, Appl
978	131.5	7.3	312	2	US-09-904-462-64	Sequence 64, Appl	1051	127.5	7.1	431	2	US-09-038-832-2	Sequence 2, Appl
979	131.5	7.3	312	2	US-09-902-736A-64	Sequence 64, Appl	1052	127.5	7.1	431	2	US-09-038-832-4	Sequence 4, Appl
980	131.5	7.3	312	2	US-09-906-722A-64	Sequence 64, Appl	1053	127.5	7.1	441	2	US-09-949-016-8211	Sequence 8211, Ap
981	131	7.3	240	1	US-08-471-570-12	Sequence 12, Appl	1054	127	7.0	383	2	US-09-949-016-11050	Sequence 11050, A
982	131	7.3	342	2	US-09-684-708A-27	Sequence 27, Appl	1055	127	7.0	917	2	US-10-282-162-54	Sequence 54, Appl
983	131	7.3	561	2	US-09-866-510-24	Sequence 24, Appl	1056	127	7.0	917	2	US-10-282-162-56	Sequence 56, Appl
984	131	7.3	782	2	US-09-684-708A-21	Sequence 21, Appl	1057	127	7.0	992	1	US-07-813-593-2	Sequence 2, Appl
985	131	7.3	1090	2	US-09-866-510-14	Sequence 14, Appl	1058	127	7.0	992	1	US-07-977-451-2	Sequence 2, Appl
986	131	7.3	1106	1	US-08-180-195-2	Sequence 2, Appl	1059	127	7.0	992	1	US-07-946-507-2	Sequence 2, Appl
987	131	7.3	1106	1	US-08-168-917-2	Sequence 2, Appl	1060	127	7.0	992	1	US-08-252-517-2	Sequence 2, Appl
988	131	7.3	1106	1	US-08-477-329-2	Sequence 2, Appl	1061	127	7.0	992	1	US-07-906-397A-2	Sequence 2, Appl
989	131	7.3	1106	1	US-08-475-458-2	Sequence 2, Appl	1062	127	7.0	992	1	US-08-601-891-2	Sequence 2, Appl
990	131	7.3	1106	1	US-08-460-510-2	Sequence 2, Appl	1063	127	7.0	992	1	US-09-021-324-2	Sequence 2, Appl
991	131	7.3	1106	1	US-08-460-490-2	Sequence 2, Appl	1064	127	7.0	992	2	US-09-872-136B-2	Sequence 2, Appl
992	131	7.3	1106	2	US-08-380-400-2	Sequence 2, Appl	1065	127	7.0	992	2	US-09-913-408A-2	Sequence 2, Appl
993	131	7.3	1106	2	US-08-462-728-4	Sequence 4, Appl	1066	127	7.0	992	4	PCT-US92-02750-2	Sequence 2, Appl
994	131	7.3	1106	2	US-09-583-459A-2	Sequence 2, Appl	1067	127	7.0	992	4	PCT-US92-05401-2	Sequence 2, Appl
995	131	7.3	1106	2	US-09-583-210-2	Sequence 2, Appl	1068	127	7.0	992	4	PCT-US92-09893-2	Sequence 2, Appl
996	131	7.3	1106	2	US-09-583-449A-2	Sequence 2, Appl	1069	126.5	7.0	352	2	US-09-991-181-505	Sequence 505, App
997	131	7.3	1106	2	US-09-435-059-2	Sequence 2, Appl	1070	126.5	7.0	352	2	US-09-990-444-505	Sequence 505, App
998	131	7.3	1106	2	US-08-461-917-4	Sequence 4, Appl	1071	126.5	7.0	352	2	US-09-997-333-505	Sequence 505, App
999	131	7.3	1106	2	US-08-464-436-4	Sequence 4, Appl	1072	126.5	7.0	352	2	US-09-992-598-505	Sequence 505, App
1000	131	7.3	1106	2	US-08-464-436-4	Sequence 4, Appl	1073	126.5	7.0	365	1	US-08-979-424-3	Sequence 3, Appl
1001	131	7.3	1106	2	US-09-866-510-16	Sequence 16, Appl	1074	126.5	7.0	365	1	US-09-272-436-2	Sequence 2, Appl
1002	131	7.3	1106	2	US-09-866-510-18	Sequence 18, Appl	1075	126.5	7.0	365	2	US-09-949-016-6064	Sequence 6064, Ap
1003	131	7.3	1106	2	US-09-866-510-20	Sequence 20, Appl	1076	126	7.0	277	2	US-09-354-151-3	Sequence 3, Appl
1004	131	7.3	1106	2	US-09-866-510-22	Sequence 22, Appl	1077	126	7.0	477	1	US-08-359-705B-4	Sequence 4, Appl
1005	131	7.3	1106	4	PCT-US92-00730-2	Sequence 2, Appl	1078	126	7.0	477	1	US-08-286-846A-4	Sequence 4, Appl
1006	131	7.3	1106	4	PCT-US92-00862-2	Sequence 2, Appl	1079	126	7.0	477	1	US-08-457-880A-4	Sequence 4, Appl
1007	130.5	7.2	291	2	US-10-027-736A-19	Sequence 19, Appl	1080	126	7.0	477	2	US-08-444-622A-4	Sequence 4, Appl
1008	130.5	7.2	298	2	US-09-152-060-76	Sequence 76, Appl	1081	126	7.0	477	2	US-08-942-562-4	Sequence 4, Appl
1009	130.5	7.2	298	2	US-09-852-797-76	Sequence 76, Appl	1082	126	7.0	477	2	US-09-156-923-4	Sequence 4, Appl
1010	130.5	7.2	298	2	US-09-853-161-76	Sequence 76, Appl	1083	126	7.0	822	1	US-08-359-705B-2	Sequence 2, Appl
1011	130.5	7.2	298	2	US-10-058-993-76	Sequence 76, Appl	1084	126	7.0	822	1	US-08-286-846A-2	Sequence 2, Appl
1012	130.5	7.2	315	2	US-09-949-016-11121	Sequence 11121, A	1085	126	7.0	822	1	US-08-457-880A-2	Sequence 2, Appl
1013	130.5	7.2	315	2	US-09-949-016-11122	Sequence 11122, A	1086	126	7.0	822	1	US-08-444-622A-2	Sequence 2, Appl
1014	130.5	7.2	432	2	US-08-477-460B-2	Sequence 2, Appl	1087	126	7.0	822	2	US-08-942-562-2	Sequence 2, Appl
1015	130.5	7.2	432	2	US-08-379-516-2	Sequence 2, Appl	1088	126	7.0	822	2	US-09-156-923-2	Sequence 2, Appl
1016	130.5	7.2	432	2	US-09-329-516-2	Sequence 2, Appl	1089	126	7.0	822	2	US-09-949-016-6698	Sequence 6698, Ap
1017	130.5	7.2	432	2	US-08-485-372A-2	Sequence 2, Appl	1090	126	7.0	847	1	US-08-286-305A-5	Sequence 5, Appl
1018	130.5	7.2	432	2	US-09-409-006A-2	Sequence 2, Appl	1091	126	7.0	847	1	US-08-441-104A-5	Sequence 5, Appl
1019	130.5	7.2	432	2	US-08-484-681-2	Sequence 2, Appl	1092	126	7.0	847	1	US-08-440-816A-5	Sequence 5, Appl
1020	130.5	7.2	432	2	US-09-766-995-2	Sequence 2, Appl	1093	126	7.0	847	2	US-09-417-381A-5	Sequence 5, Appl
1021	130.5	7.2	432	4	PCT-US93-07422-2	Sequence 2, Appl	1094	126	7.0	1000	1	US-08-222-239-2	Sequence 2, Appl
1022	130.5	7.2	466	2	US-09-604-107A-8	Sequence 8, Appl	1095	126	7.0	1000	1	US-08-434-878-2	Sequence 2, Appl
1023	130	7.2	249	2	US-09-336-536-42	Sequence 42, Appl	1096	126	7.0	1000	4	PCT-US95-03718-2	Sequence 2, Appl
1024	130	7.2	259	2	US-10-104-047-2303	Sequence 2303, Ap	1097	125.5	6.9	365	2	US-08-928-383B-2	Sequence 2, Appl
1025	130	7.2	394	2	US-09-336-536-39	Sequence 39, Appl	1098	125.5	6.9	518	2	US-09-919-172-20	Sequence 20, Appl
1026	130	7.2	802	2	US-09-173-151A-33	Sequence 33, Appl	1099	125.5	6.9	526	2	US-09-910-174B-9	Sequence 9, Appl
1027	129.5	7.2	728	1	US-07-912-952-4	Sequence 4, Appl	1100	125.5	6.9	526	2	US-09-620-461-9	Sequence 9, Appl
1028	129	7.1	340	2	US-09-188-930-184	Sequence 184, App	1101	125.5	6.9	526	2	US-09-949-016-6122	Sequence 6122, Ap
1029	129	7.1	340	2	US-09-312-283C-184	Sequence 184, App	1102	125.5	6.9	540	2	US-09-949-016-11644	Sequence 11644, A
1030	129	7.1	417	2	US-09-949-016-6729	Sequence 6729, Ap	1103	125.5	6.9	589	1	US-08-724-394A-1	Sequence 1, Appl
1031	129	7.1	456	2	US-09-949-016-7554	Sequence 7554, Ap	1104	125	6.9	391	4	PCT-US95-15696-2	Sequence 2, Appl
1032	128	7.1	341	2	US-09-336-536-29	Sequence 29, Appl	1105	124.5	6.9	241	2	US-08-341-018-54	Sequence 54, Appl
1033	128	7.1	370	2	US-09-336-536-28	Sequence 28, Appl	1106	124.5	6.9	241	2	US-08-470-335-195	Sequence 195, App
1034	128	7.1	483	1	US-08-392-338A-19	Sequence 19, Appl	1107	124.5	6.9	241	2	US-08-470-339-195	Sequence 195, App
1035	128	7.1	483	2	US-09-166-750-19	Sequence 19, Appl	1108	124.5	6.9	241	2	US-08-467-602-389	Sequence 389, App
1036	128	7.1	483	2	US-09-166-093-19	Sequence 19, Appl	1109	124.5	6.9	731	1	US-08-411-295F-47	Sequence 47, Appl
1037	128	7.1	483	2	US-09-172-019-19	Sequence 19, Appl	1110	124.5	6.9	731	1	US-08-070-165F-10	Sequence 10, Appl
1038	128	7.1	483	2	US-09-166-094-19	Sequence 19, Appl	1111	124.5	6.9	731	1	US-08-885-418-10	Sequence 10, Appl
1039	128	7.1	483	2	US-09-443-213-19	Sequence 19, Appl	1112	124	6.9	198	2	US-08-885-418-10	Sequence 34, Appl
1040	128	7.1	483	2	US-09-949-016-8574	Sequence 8574, Ap	1113	124	6.9	637	2	US-09-569-611C-35	Sequence 35, Appl
1041	128	7.1	795	2	US-09-949-016-71119	Sequence 7119, Ap	1114	124	6.9	665	2	US-09-942-711-16	Sequence 16, Appl
1042	128	7.1	806	2	US-09-383-630-3	Sequence 3, Appl	1115	124	6.9	983	2	US-09-942-711-19	Sequence 19, Appl
1043	127.5	7.1	100	2	US-08-411-295F-121	Sequence 121, App	1116	124	6.9	986	2	US-09-942-711-18	Sequence 18, Appl
1044	127.5	7.1	206	2	US-08-341-018-2	Sequence 2, Appl	1117	124	6.9	986	2	US-09-942-711-20	Sequence 20, Appl
1045	127.5	7.1	206	2	US-08-470-335-190	Sequence 190, App	1118	124	6.9	993	1	US-07-977-451-4	Sequence 4, Appl
1046	127.5	7.1	206	2	US-08-470-339-190	Sequence 190, App	1119	124	6.9	993	1	US-08-252-517-4	Sequence 4, Appl
1047	127.5	7.1	206	2	US-08-467-602-383	Sequence 383, App	1120	124	6.9	993	1	US-07-906-397A-4	Sequence 4, Appl
1048	127.5	7.1	206	2	US-08-411-295F-2	Sequence 2, Appl	1121	124	6.9	993	1	US-08-601-891-4	Sequence 4, Appl
1049	127.5	7.1	206	2	US-08-411-295F-76	Sequence 76, Appl	1122	124	6.9	993	1	US-09-021-324-4	Sequence 4, Appl

1123	124	6.9	993	2	US-09-872-136B-4	Sequence 4, Appli	1196	122.5	6.8	418	2	US-08-467-603-230	Sequence 230, App
1124	124	6.9	993	2	US-09-919-408A-4	Sequence 4, Appli	1197	122.5	6.8	418	2	US-08-411-295F-156	Sequence 156, App
1125	124	6.9	993	2	PCT-US92-09893-4	Sequence 4, Appli	1198	122.5	6.8	420	2	US-08-467-602-260	Sequence 260, App
1126	124	6.9	994	2	US-09-942-711-17	Sequence 17, Appli	1199	122.5	6.8	420	2	US-08-411-295F-186	Sequence 186, App
1127	124	6.9	999	1	US-08-252-626A-2	Sequence 2, Appli	1200	122.5	6.8	422	2	US-08-753-007A-9	Sequence 9, Appli
1128	124	6.9	999	1	US-09-949-016-6718	Sequence 6718, Ap	1201	122.5	6.8	422	2	US-09-398-496-9	Sequence 9, Appli
1129	124	6.9	1160	4	PCT-US92-05401-4	Sequence 4, Appli	1202	122.5	6.8	423	2	US-08-467-602-255	Sequence 255, App
1130	123.5	6.8	156	2	US-08-467-602-381	Sequence 381, App	1203	122.5	6.8	423	2	US-08-411-295F-181	Sequence 181, App
1131	123.5	6.8	156	2	US-08-411-295F-306	Sequence 306, App	1204	122.5	6.8	429	2	US-08-467-603-269	Sequence 269, App
1132	123.5	6.8	241	1	US-07-847-743B-30	Sequence 30, Appli	1205	122.5	6.8	429	2	US-08-411-295F-195	Sequence 195, App
1133	123.5	6.8	241	1	US-08-456-201-30	Sequence 30, Appli	1206	122.5	6.8	432	2	US-08-467-602-266	Sequence 266, App
1134	123.5	6.8	241	1	US-08-456-241-30	Sequence 30, Appli	1207	122.5	6.8	432	2	US-08-411-295F-192	Sequence 192, App
1135	123.5	6.8	241	4	PCT-US92-04295A-30	Sequence 30, Appli	1208	122.5	6.8	432	2	US-08-467-602-263	Sequence 263, App
1136	123.5	6.8	357	2	US-10-027-736A-9	Sequence 9, Appli	1209	122.5	6.8	443	2	US-08-411-295F-189	Sequence 189, App
1137	123.5	6.8	420	1	US-07-847-743B-29	Sequence 29, Appli	1210	122.5	6.8	452	2	US-08-467-603-272	Sequence 272, App
1138	123.5	6.8	420	1	US-08-456-201-29	Sequence 29, Appli	1211	122.5	6.8	452	2	US-08-411-295F-198	Sequence 198, App
1139	123.5	6.8	420	1	US-08-456-241-29	Sequence 29, Appli	1212	122.5	6.8	603	2	US-08-467-602-216	Sequence 216, App
1140	123.5	6.8	420	4	PCT-US92-04295A-29	Sequence 29, Appli	1213	122.5	6.8	603	2	US-08-411-295F-142	Sequence 142, App
1141	123.5	6.8	637	1	US-07-847-743B-28	Sequence 28, Appli	1214	122.5	6.8	606	2	US-08-467-602-214	Sequence 214, App
1142	123.5	6.8	637	1	US-08-456-201-28	Sequence 28, Appli	1215	122.5	6.8	606	2	US-08-411-295F-140	Sequence 140, App
1143	123.5	6.8	637	1	US-08-456-241-28	Sequence 28, Appli	1216	122.5	6.8	612	2	US-08-467-602-228	Sequence 228, App
1144	123.5	6.8	637	4	PCT-US92-04295A-28	Sequence 28, Appli	1217	122.5	6.8	612	2	US-08-411-295F-154	Sequence 154, App
1145	123.5	6.8	645	1	US-07-847-743B-27	Sequence 27, Appli	1218	122.5	6.8	615	2	US-08-467-602-225	Sequence 225, App
1146	123.5	6.8	645	1	US-08-456-201-27	Sequence 27, Appli	1219	122.5	6.8	615	2	US-08-411-295F-151	Sequence 151, App
1147	123.5	6.8	645	1	US-08-428-926-4	Sequence 4, Appli	1220	122.5	6.8	625	1	US-07-847-743B-26	Sequence 26, Appli
1148	123.5	6.8	645	1	US-08-428-927-4	Sequence 4, Appli	1221	122.5	6.8	625	1	US-08-456-201-26	Sequence 26, Appli
1149	123.5	6.8	645	1	US-08-428-998-4	Sequence 4, Appli	1222	122.5	6.8	625	4	PCT-US92-04295A-26	Sequence 26, Appli
1150	123.5	6.8	645	1	US-08-339-517-4	Sequence 4, Appli	1223	122.5	6.8	626	2	US-08-467-602-222	Sequence 222, App
1151	123.5	6.8	645	1	US-08-456-241-27	Sequence 27, Appli	1224	122.5	6.8	626	2	US-08-411-295F-148	Sequence 148, App
1152	123.5	6.8	645	2	US-09-020-880-93	Sequence 93, Appli	1225	122.5	6.8	635	2	US-08-467-602-231	Sequence 231, App
1153	123.5	6.8	645	2	US-09-101-544-93	Sequence 93, Appli	1226	122.5	6.8	635	2	US-08-411-295F-157	Sequence 157, App
1154	123.5	6.8	645	2	US-09-097-681-3	Sequence 3, Appli	1227	122.5	6.8	637	2	US-08-467-602-258	Sequence 258, App
1155	123.5	6.8	645	4	PCT-US92-04295A-27	Sequence 27, Appli	1228	122.5	6.8	637	2	US-08-411-295F-184	Sequence 184, App
1156	123.5	6.8	732	1	US-07-847-743B-9	Sequence 9, Appli	1229	122.5	6.8	640	2	US-08-467-602-256	Sequence 256, App
1157	123.5	6.8	732	1	US-08-456-201-9	Sequence 9, Appli	1230	122.5	6.8	640	2	US-08-411-295F-182	Sequence 182, App
1158	123.5	6.8	732	4	PCT-US92-04295A-9	Sequence 9, Appli	1231	122.5	6.8	645	2	US-08-753-007A-10	Sequence 10, Appli
1159	123.5	6.8	732	4	US-08-456-241-9	Sequence 9, Appli	1232	122.5	6.8	645	2	US-09-398-496-10	Sequence 10, Appli
1160	123	6.8	321	2	US-09-254-465A-2	Sequence 2, Appli	1233	122.5	6.8	646	2	US-08-467-602-270	Sequence 270, App
1161	123	6.8	321	2	US-09-953-499-2	Sequence 2, Appli	1234	122.5	6.8	646	2	US-08-411-295F-196	Sequence 196, App
1162	123	6.8	321	2	US-09-999-833A-52	Sequence 52, Appli	1235	122.5	6.8	646	2	US-08-467-602-267	Sequence 267, App
1163	123	6.8	321	2	US-10-020-445A-52	Sequence 52, Appli	1236	122.5	6.8	649	2	US-08-411-295F-193	Sequence 193, App
1164	123	6.8	354	6	5169835-4	Patent No. 5169835	1237	122.5	6.8	649	2	US-08-411-295F-155	Sequence 155, App
1165	123	6.8	553	1	US-08-263-911-9	Sequence 35, Appli	1238	122.5	6.8	650	2	US-08-467-602-217	Sequence 217, App
1166	123	6.8	668	2	US-09-173-151A-35	Sequence 35, Appli	1239	122.5	6.8	650	2	US-08-411-295F-143	Sequence 143, App
1167	123	6.8	821	1	US-08-339-578-2	Sequence 2, Appli	1240	122.5	6.8	653	2	US-08-467-602-212	Sequence 212, App
1168	122.5	6.8	133	2	US-08-467-602-380	Sequence 380, App	1241	122.5	6.8	653	2	US-08-411-295F-138	Sequence 138, App
1169	122.5	6.8	161	1	US-08-096-277-18	Sequence 18, Appli	1242	122.5	6.8	659	2	US-08-467-602-229	Sequence 229, App
1170	122.5	6.8	161	1	US-08-550-815-18	Sequence 18, Appli	1243	122.5	6.8	659	2	US-08-411-295F-155	Sequence 155, App
1171	122.5	6.8	161	2	US-08-703-089-18	Sequence 18, Appli	1244	122.5	6.8	660	2	US-08-467-602-264	Sequence 264, App
1172	122.5	6.8	207	2	US-08-467-602-219	Sequence 219, App	1245	122.5	6.8	660	2	US-08-411-295F-190	Sequence 190, App
1173	122.5	6.8	207	2	US-08-411-295F-145	Sequence 145, App	1246	122.5	6.8	662	2	US-08-467-602-226	Sequence 226, App
1174	122.5	6.8	210	2	US-08-467-602-215	Sequence 215, App	1247	122.5	6.8	662	2	US-08-411-295F-152	Sequence 152, App
1175	122.5	6.8	210	2	US-08-411-295F-141	Sequence 141, App	1248	122.5	6.8	669	1	US-07-847-743B-8	Sequence 8, Appli
1176	122.5	6.8	230	2	US-08-467-602-223	Sequence 223, App	1249	122.5	6.8	669	1	US-08-440-401-11	Sequence 11, Appli
1177	122.5	6.8	230	2	US-08-411-295F-149	Sequence 149, App	1250	122.5	6.8	669	1	US-08-456-201-8	Sequence 8, Appli
1178	122.5	6.8	241	2	US-08-467-602-261	Sequence 261, App	1251	122.5	6.8	669	1	US-08-330-161-11	Sequence 11, Appli
1179	122.5	6.8	241	2	US-08-411-295F-187	Sequence 187, App	1252	122.5	6.8	669	1	US-08-456-241-8	Sequence 8, Appli
1180	122.5	6.8	244	2	US-08-467-602-257	Sequence 257, App	1253	122.5	6.8	669	1	US-08-456-241-13	Sequence 13, Appli
1181	122.5	6.8	244	2	US-08-411-295F-183	Sequence 183, App	1254	122.5	6.8	669	1	US-08-440-401-11	Sequence 11, Appli
1182	122.5	6.8	264	2	US-08-467-602-265	Sequence 265, App	1255	122.5	6.8	669	1	US-08-419-878B-11	Sequence 11, Appli
1183	122.5	6.8	264	2	US-08-411-295F-191	Sequence 191, App	1256	122.5	6.8	669	2	US-09-173-480-11	Sequence 11, Appli
1184	122.5	6.8	281	2	US-10-027-736A-67	Sequence 67, Appli	1257	122.5	6.8	669	2	US-08-467-602-273	Sequence 273, App
1185	122.5	6.8	316	2	US-10-027-736A-17	Sequence 17, Appli	1258	122.5	6.8	669	2	US-08-411-295F-199	Sequence 199, App
1186	122.5	6.8	386	2	US-08-467-602-218	Sequence 218, App	1259	122.5	6.8	669	2	US-10-022-609-11	Sequence 11, Appli
1187	122.5	6.8	386	2	US-08-411-295F-144	Sequence 144, App	1260	122.5	6.8	669	4	PCT-US92-04295A-8	Sequence 8, Appli
1188	122.5	6.8	389	2	US-08-467-602-213	Sequence 213, App	1261	122.5	6.8	669	4	PCT-US92-04295A-13	Sequence 13, Appli
1189	122.5	6.8	389	2	US-08-411-295F-139	Sequence 139, App	1262	122.5	6.8	673	2	US-08-467-602-220	Sequence 220, App
1190	122.5	6.8	395	2	US-08-467-602-227	Sequence 227, App	1263	122.5	6.8	673	2	US-08-411-295F-146	Sequence 146, App
1191	122.5	6.8	395	2	US-08-411-295F-153	Sequence 153, App	1264	122.5	6.8	682	2	US-08-467-602-232	Sequence 232, App
1192	122.5	6.8	398	2	US-08-467-602-224	Sequence 224, App	1265	122.5	6.8	682	2	US-08-411-295F-158	Sequence 158, App
1193	122.5	6.8	398	2	US-08-411-295F-150	Sequence 150, App	1266	122.5	6.8	684	2	US-08-467-602-259	Sequence 259, App
1194	122.5	6.8	409	2	US-08-467-602-221	Sequence 221, App	1267	122.5	6.8	684	2	US-08-411-295F-185	Sequence 185, App
1195	122.5	6.8	409	2	US-08-411-295F-147	Sequence 147, App	1268	122.5	6.8	684	2		

1269	122.5	6.8	687	2	US-08-467-602-254	Sequence 254, App	1342	119.5	6.6	450	2	US-09-906-618-320	Sequence 320, App
1270	122.5	6.8	687	2	US-08-411-2959-180	Sequence 180, App	1343	119.5	6.6	450	2	US-09-906-646-320	Sequence 320, App
1271	122.5	6.8	693	2	US-08-467-602-271	Sequence 271, App	1344	119.5	6.6	450	2	US-09-904-462-320	Sequence 320, App
1272	122.5	6.8	693	2	US-08-411-2959-197	Sequence 197, App	1345	119.5	6.6	450	2	US-09-902-736A-320	Sequence 320, App
1273	122.5	6.8	696	2	US-08-467-602-268	Sequence 268, App	1346	119.5	6.6	450	2	US-09-906-722A-320	Sequence 320, App
1274	122.5	6.8	696	2	US-08-411-2959-194	Sequence 194, App	1347	119.5	6.6	477	2	US-09-949-016-9192	Sequence 9192, Ap
1275	122.5	6.8	707	2	US-08-467-602-262	Sequence 262, App	1348	119.5	6.6	477	2	US-09-949-016-9193	Sequence 9193, Ap
1276	122.5	6.8	707	2	US-08-411-2959-188	Sequence 188, App	1349	119.5	6.6	477	2	US-09-949-016-9194	Sequence 9194, Ap
1277	122.5	6.8	716	2	US-08-467-602-274	Sequence 274, App	1350	119.5	6.6	477	2	US-09-949-016-9195	Sequence 9195, Ap
1278	122.5	6.8	716	2	US-08-411-2959-200	Sequence 200, App	1351	119.5	6.6	477	2	US-09-949-016-9196	Sequence 9196, Ap
1279	122	6.8	146	2	US-09-270-767-33187	Sequence 33187, A	1352	119.5	6.6	477	2	US-09-949-016-9197	Sequence 9197, Ap
1280	122	6.8	298	2	US-09-864-675-4	Sequence 4, Appli	1353	119.5	6.6	477	2	US-09-949-016-9198	Sequence 9198, Ap
1281	122	6.8	330	2	US-09-864-675-2	Sequence 2, Appli	1354	119.5	6.6	477	2	US-09-949-016-9199	Sequence 9199, Ap
1282	122	6.8	337	2	US-09-949-016-9074	Sequence 9074, Ap	1355	119.5	6.6	505	2	US-09-240-915-3	Sequence 3, Appli
1283	122	6.8	352	2	US-09-949-016-9074	Sequence 1040, A	1356	119.5	6.6	505	2	US-09-591-435-3	Sequence 3, Appli
1284	122	6.8	365	2	US-09-949-016-9075	Sequence 9075, Ap	1357	119.5	6.6	505	2	US-10-098-600B-3	Sequence 3, Appli
1285	122	6.8	371	2	US-09-949-016-9073	Sequence 9073, Ap	1358	119	6.6	261	2	US-09-899-634C-2	Sequence 2, Appli
1286	122	6.8	407	2	US-10-104-047-3074	Sequence 3074, Ap	1359	119	6.6	330	1	US-08-525-864A-4	Sequence 4, Appli
1287	122	6.8	421	2	US-09-569-611C-36	Sequence 36, Appl	1360	119	6.6	365	2	US-09-899-634C-4	Sequence 4, Appli
1288	122	6.8	469	2	US-08-753-007A-8	Sequence 8, Appli	1361	119	6.6	754	1	US-08-525-864A-2	Sequence 2, Appli
1289	122	6.8	469	2	US-09-398-496-8	Sequence 8, Appli	1362	119	6.6	910	2	US-09-313-942-28	Sequence 28, Appl
1290	122	6.8	548	2	US-09-548-473B-8	Sequence 8, Appli	1363	119	6.6	910	2	US-10-282-162-28	Sequence 28, Appl
1291	122	6.8	647	2	US-08-753-007A-32	Sequence 32, Appl	1364	119	6.6	969	2	US-09-949-016-8059	Sequence 8059, Ap
1292	122	6.8	647	2	US-09-398-496-32	Sequence 32, Appl	1365	118.5	6.6	553	1	US-08-263-911-7	Sequence 7, Appli
1293	122	6.8	915	2	US-10-282-162-52	Sequence 52, Appl	1366	118.5	6.6	668	2	US-09-949-016-8139	Sequence 8139, Ap
1294	121.5	6.7	231	1	US-08-168-091A-4	Sequence 4, Appli	1367	118.5	6.6	931	2	US-10-037-417-118	Sequence 118, App
1295	121.5	6.7	286	2	US-09-270-767-44618	Sequence 44618, A	1368	118.5	6.6	931	2	US-10-037-417-119	Sequence 119, App
1296	121.5	6.7	317	2	US-10-104-047-3036	Sequence 3036, Ap	1369	118.5	6.6	931	2	US-10-037-417-120	Sequence 120, App
1297	121.5	6.7	390	1	US-08-979-424-1	Sequence 1, Appli	1370	118.5	6.6	2860	1	US-08-826-267-2	Sequence 2, Appli
1298	121.5	6.7	390	2	US-09-907-794A-39	Sequence 39, Appl	1371	118	6.5	300	1	US-07-640-029-5	Sequence 5, Appli
1299	121.5	6.7	390	2	US-09-905-125A-39	Sequence 39, Appl	1372	118	6.5	300	2	US-08-439-992A-5	Sequence 5, Appli
1300	121.5	6.7	390	2	US-09-902-775A-39	Sequence 39, Appl	1373	118	6.5	300	2	US-09-620-561-5	Sequence 5, Appli
1301	121.5	6.7	390	2	US-09-906-700-39	Sequence 39, Appl	1374	118	6.5	993	1	US-08-222-299-4	Sequence 4, Appli
1302	121.5	6.7	390	2	US-09-903-603A-39	Sequence 39, Appl	1375	118	6.5	993	1	US-08-434-878-4	Sequence 4, Appli
1303	121.5	6.7	390	2	US-09-904-920A-39	Sequence 39, Appl	1376	118	6.5	993	4	PCT-US95-03718-4	Sequence 4, Appli
1304	121.5	6.7	390	2	US-09-909-064-39	Sequence 39, Appl	1377	117.5	6.5	191	2	US-09-270-767-33678	Sequence 33678, A
1305	121.5	6.7	390	2	US-09-905-381A-39	Sequence 39, Appl	1378	117.5	6.5	191	2	US-09-270-767-48895	Sequence 48895, A
1306	121.5	6.7	390	2	US-09-906-618-39	Sequence 39, Appl	1379	117.5	6.5	246	2	US-09-336-536-31	Sequence 31, Appl
1307	121.5	6.7	390	2	US-09-906-646-39	Sequence 39, Appl	1380	117.5	6.5	336	1	US-07-904-073-2	Sequence 2, Appli
1308	121.5	6.7	390	2	US-09-904-462-39	Sequence 39, Appl	1381	117.5	6.5	336	1	US-07-904-071-2	Sequence 2, Appli
1309	121.5	6.7	390	2	US-09-902-736A-39	Sequence 39, Appl	1382	117.5	6.5	336	1	US-08-442-043A-16	Sequence 16, Appl
1310	121.5	6.7	390	2	US-09-906-722A-39	Sequence 39, Appl	1383	117.5	6.5	336	2	US-08-441-893A-16	Sequence 16, Appl
1311	121	6.7	302	1	US-07-921-807B-7	Sequence 7, Appli	1384	117.5	6.5	336	2	US-10-027-736A-65	Sequence 65, Appl
1312	121	6.7	302	1	US-08-441-944A-7	Sequence 7, Appli	1385	117.5	6.5	365	2	US-09-336-536-40	Sequence 40, Appl
1313	121	6.7	315	2	US-09-310-174B-28	Sequence 28, Appl	1386	117.5	6.5	569	1	US-07-821-716-2	Sequence 2, Appli
1314	121	6.7	315	2	US-09-620-461-28	Sequence 28, Appl	1387	117.5	6.5	569	1	US-08-381-603-2	Sequence 2, Appli
1315	121	6.7	900	2	US-10-282-162-40	Sequence 40, Appl	1388	117.5	6.5	569	2	US-08-924-376-2	Sequence 2, Appli
1316	121	6.7	902	2	US-10-282-162-42	Sequence 42, Appl	1389	117.5	6.5	569	2	US-08-685-212-2	Sequence 2, Appli
1317	121	6.7	902	2	US-10-282-162-44	Sequence 44, Appl	1390	117.5	6.5	569	2	US-09-173-151A-31	Sequence 31, Appl
1318	120.5	6.7	165	1	US-08-168-091A-33	Sequence 33, Appl	1391	117.5	6.5	569	2	US-08-466-932A-6	Sequence 2, Appli
1319	120.5	6.7	197	2	US-08-833-488B-4	Sequence 4, Appli	1392	117.5	6.5	569	2	US-08-408-842A-6	Sequence 6, Appli
1320	120.5	6.7	197	2	US-08-833-488B-9	Sequence 9, Appli	1393	117.5	6.5	569	2	US-09-949-016-6000	Sequence 6000, Ap
1321	120.5	6.7	236	6	5455030-7	Patent No. 5455030	1394	117.5	6.5	569	4	PCT-US94-02414-2	Sequence 2, Appli
1322	120.5	6.7	548	2	US-09-548-473B-9	Sequence 9, Appli	1395	117.5	6.5	569	4	PCT-US96-08899-2	Sequence 2, Appli
1323	120.5	6.7	915	2	US-10-282-162-46	Sequence 46, Appl	1396	117.5	6.5	588	2	US-09-949-016-8572	Sequence 8572, Ap
1324	120.5	6.7	917	2	US-10-282-162-48	Sequence 48, Appl	1397	117.5	6.5	900	2	US-10-282-162-34	Sequence 34, Appl
1325	120.5	6.7	917	2	US-10-282-162-50	Sequence 50, Appl	1398	117.5	6.5	902	2	US-10-282-162-36	Sequence 36, Appl
1326	120	6.6	193	2	US-09-397-2430-4	Sequence 4, Appli	1399	117.5	6.5	902	2	US-10-282-162-38	Sequence 38, Appl
1327	120	6.6	205	2	US-09-462-270-4	Sequence 4, Appli	1400	117	6.5	264	2	US-09-270-767-33115	Sequence 33115, A
1328	120	6.6	328	2	US-09-949-016-6428	Sequence 6428, Ap	1401	117	6.5	264	2	US-09-270-767-48332	Sequence 48332, A
1329	120	6.6	339	2	US-09-149-476-483	Sequence 483, App	1402	117	6.5	407	2	US-08-753-007A-6	Sequence 6, Appli
1330	120	6.6	332	2	US-09-949-016-7327	Sequence 7327, Ap	1403	117	6.5	407	2	US-09-398-496-6	Sequence 6, Appli
1331	120	6.6	361	2	US-09-270-767-45128	Sequence 45128, A	1404	117	6.5	708	2	US-09-131-648-2	Sequence 2, Appli
1332	119.5	6.6	197	2	US-08-833-488B-28	Sequence 28, Appl	1405	117	6.5	708	2	US-09-907-794A-69	Sequence 69, Appl
1333	119.5	6.6	253	2	US-08-833-488B-20	Sequence 20, Appl	1406	117	6.5	708	2	US-09-905-135A-69	Sequence 69, Appl
1334	119.5	6.6	450	2	US-09-907-794A-320	Sequence 320, App	1407	117	6.5	708	2	US-09-902-775A-69	Sequence 69, Appl
1335	119.5	6.6	450	2	US-09-905-125A-320	Sequence 320, App	1408	117	6.5	708	2	US-09-906-700-69	Sequence 69, Appl
1336	119.5	6.6	450	2	US-09-902-775A-320	Sequence 320, App	1409	117	6.5	708	2	US-09-903-603A-69	Sequence 69, Appl
1337	119.5	6.6	450	2	US-09-906-700-320	Sequence 320, App	1410	117	6.5	708	2	US-09-904-920A-69	Sequence 69, Appl
1338	119.5	6.6	450	2	US-09-903-603A-320	Sequence 320, App	1411	117	6.5	708	2	US-09-909-064-69	Sequence 69, Appl
1339	119.5	6.6	450	2	US-09-904-920A-320	Sequence 320, App	1412	117	6.5	708	2	US-09-905-381A-69	Sequence 69, Appl
1340	119.5	6.6	450	2	US-09-909-064-320	Sequence 320, App	1413	117	6.5	708	2	US-09-906-618-69	Sequence 69, Appl
1341	119.5	6.6	450	2	US-09-905-381A-320	Sequence 320, App	1414	117	6.5	708	2	US-09-906-646-69	Sequence 69, Appl

1415	117	6.5	708	2	US-09-904-462-69	Sequence 69, Appl
1416	117	6.5	708	2	US-09-902-736A-69	Sequence 69, Appl
1417	117	6.5	708	2	US-09-906-722A-69	Sequence 69, Appl
1418	117	6.5	729	1	US-07-640-029-3	Sequence 3, Appl
1419	117	6.5	733	1	US-07-640-029-4	Sequence 4, Appl
1420	117	6.5	733	1	US-07-921-807B-6	Sequence 6, Appl
1421	117	6.5	733	1	US-08-441-944A-6	Sequence 6, Appl
1422	117	6.5	733	1	US-08-439-992A-6	Sequence 6, Appl
1423	117	6.5	733	2	US-09-620-561-4	Sequence 4, Appl
1424	117	6.5	825	1	US-07-912-952-2	Sequence 2, Appl
1425	117	6.5	871	2	US-09-548-473B-7	Sequence 7, Appl
1426	117	6.5	885	1	US-08-372-892-4	Sequence 4, Appl
1427	117	6.5	885	2	US-09-919-497-52	Sequence 52, Appl
1428	117	6.5	894	1	US-08-372-892-2	Sequence 2, Appl
1429	117	6.5	894	1	US-08-445-640-34	Sequence 34, Appl
1430	117	6.5	894	2	US-08-170-558-34	Sequence 34, Appl
1431	117	6.5	894	2	US-08-447-314-34	Sequence 34, Appl
1432	117	6.5	894	2	US-08-445-461-34	Sequence 34, Appl
1433	117	6.5	894	2	US-09-223-490-34	Sequence 34, Appl
1434	117	6.5	975	2	US-09-949-016-7595	Sequence 7595, Ap
1435	117	6.5	1351	2	US-09-548-473B-1	Sequence 1, Appl
1436	117	6.5	1610	2	US-09-548-473B-4	Sequence 4, Appl
1437	117	6.5	1665	2	US-09-858-664A-2	Sequence 2, Appl
1438	117	6.5	1665	2	US-10-274-978-2	Sequence 2, Appl
1439	117	6.5	1665	2	US-10-697-263-2	Sequence 2, Appl
1440	116.5	6.5	307	1	US-08-332-562A-83	Sequence 83, Appl
1441	116.5	6.5	315	2	US-09-949-016-7014	Sequence 7014, Ap
1442	116.5	6.5	317	2	US-10-027-736B-16	Sequence 16, Appl
1443	116.5	6.5	680	2	US-08-227-496C-15	Sequence 15, Appl
1444	116.5	6.5	1060	2	US-09-419-788-19	Sequence 19, Appl
1445	116	6.4	139	2	US-08-833-488B-14	Sequence 14, Appl
1446	116	6.4	731	1	US-07-921-807B-5	Sequence 5, Appl
1447	116	6.4	731	1	US-08-441-944A-5	Sequence 5, Appl
1448	116	6.4	731	2	US-08-439-992A-3	Sequence 3, Appl
1449	116	6.4	731	2	US-09-620-561-3	Sequence 3, Appl
1450	116	6.4	879	1	US-08-554-612C-1	Sequence 1, Appl
1451	116	6.4	993	1	US-08-183-211-2	Sequence 2, Appl
1452	116	6.4	993	4	PCT-US95-00176A-2	Sequence 2, Appl
1453	115.5	6.4	173	2	US-08-833-488B-31	Sequence 31, Appl
1454	115.5	6.4	229	2	US-08-833-488B-24	Sequence 24, Appl
1455	115.5	6.4	248	1	US-08-323-445A-6	Sequence 6, Appl
1456	115.5	6.4	248	1	US-08-515-903A-6	Sequence 6, Appl
1457	115.5	6.4	248	4	PCT-US95-12840-6	Sequence 6, Appl
1458	115.5	6.4	530	2	US-08-477-460B-4	Sequence 4, Appl
1459	115.5	6.4	530	2	US-08-379-516-4	Sequence 4, Appl
1460	115.5	6.4	530	2	US-09-329-916-4	Sequence 4, Appl
1461	115.5	6.4	530	2	US-08-485-372A-4	Sequence 4, Appl
1462	115.5	6.4	530	2	US-09-409-006A-4	Sequence 4, Appl
1463	115.5	6.4	530	2	US-08-484-681-4	Sequence 4, Appl
1464	115.5	6.4	530	2	US-09-766-995-4	Sequence 4, Appl
1465	115.5	6.4	530	4	PCT-US93-07422-4	Sequence 4, Appl
1466	115	6.4	318	6	5223394-11	Patent No. 5223394
1467	114.5	6.3	139	1	US-08-168-091A-35	Sequence 35, Appl
1468	114.5	6.3	365	2	US-08-928-383B-23	Sequence 23, Appl
1469	114.5	6.3	365	2	US-08-928-383B-24	Sequence 24, Appl
1470	114.5	6.3	374	2	US-10-027-736A-10	Sequence 10, Appl
1471	114.5	6.3	455	2	US-09-949-016-6949	Sequence 6949, Ap
1472	114	6.3	294	2	US-10-027-736A-18	Sequence 18, Appl
1473	114	6.3	302	1	US-07-640-029-6	Sequence 6, Appl
1474	114	6.3	302	1	US-07-921-807B-8	Sequence 8, Appl
1475	114	6.3	302	1	US-08-441-944A-8	Sequence 8, Appl
1476	114	6.3	302	2	US-08-439-992A-6	Sequence 6, Appl
1477	114	6.3	302	2	US-09-620-561-6	Sequence 6, Appl
1478	114	6.3	467	2	US-09-046-736-2	Sequence 2, Appl
1479	113.5	6.3	262	1	US-08-323-445A-4	Sequence 4, Appl
1480	113.5	6.3	262	1	US-08-515-903A-4	Sequence 4, Appl
1481	113.5	6.3	262	4	PCT-US95-12840-6	Sequence 6, Appl
1482	113.5	6.3	307	2	US-08-956-338-25	Sequence 25, Appl
1483	113.5	6.3	307	2	US-09-556-972-25	Sequence 25, Appl
1484	113.5	6.3	455	2	US-09-949-016-11026	Sequence 11026, A
1485	113.5	6.3	518	2	US-09-240-915-8	Sequence 8, Appl
1486	113.5	6.3	518	2	US-09-591-435-8	Sequence 8, Appl
1487	113.5	6.3	518	2	US-10-098-600B-8	Sequence 8, Appl

RESULT 2

1488 113.5 6.3 519 2 US-08-996-338-21 Sequence 21, Appl
1489 113.5 6.3 519 2 US-09-556-972-21 Sequence 21, Appl
1490 113.5 6.3 537 1 US-08-604-333-4 Sequence 4, Appl
1491 113.5 6.3 537 2 US-09-110-618-4 Sequence 4, Appl
1492 113.5 6.3 537 2 US-09-173-151A-29 Sequence 29, Appl
1493 113.5 6.3 537 2 US-09-578-178-4 Sequence 4, Appl
1494 113.5 6.3 537 2 US-09-577-806-4 Sequence 4, Appl
1495 113.5 6.3 537 2 US-09-621-502-8 Sequence 8, Appl
1496 113.5 6.3 547 1 US-08-473-981A-6 Sequence 6, Appl
1497 113.5 6.3 547 1 US-08-474-087-6 Sequence 6, Appl
1498 113 6.3 273 2 US-09-270-767-32843 Sequence 32843, A
1499 113 6.3 273 2 US-09-270-767-48060 Sequence 48060, A
1500 113 6.3 278 2 US-09-270-767-42034 Sequence 42034, A

ALIGNMENTS

RESULT 1
US-09-700-397-3
; Sequence 3, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
US-09-700-397-3

Query Match 100.0%; Score 1806; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-172;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKTIQPMHNSISWAI	FTGLAALCLFQGVPRSGDATFPKAMDNTVTRQGESATLRCTID	60
Db	1	MKTIQPMHNSISWAI	FTGLAALCLFQGVPRSGDATFPKAMDNTVTRQGESATLRCTID	60
Qy	61	NRVTRVAVLNRS	TILYAGNDKWCCLDRVLLSNTQYISIEIONVDYDEGPTCSVQTD	120
Db	61	NRVTRVAVLNRS	TILYAGNDKWCCLDRVLLSNTQYISIEIONVDYDEGPTCSVQTD	120
Qy	121	NHPKTSRVHLIVQVSPK	IVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV	180
Db	121	NHPKTSRVHLIVQVSPK	IVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFV	180
Qy	181	SEDEYLEIOG	ITREQSGDYECSSASNDVAAPVVRVRRVKVTNNYPPIYI	240
Db	181	SEDEYLEIOG	ITREQSGDYECSSASNDVAAPVVRVRRVKVTNNYPPIYI	240
Qy	241	LQCEASAVPSAE	PQWTKDKRLIEGKKGVKVENRPFSLKLI	300
Db	241	LQCEASAVPSAE	PQWTKDKRLIEGKKGVKVENRPFSLKLI	300
Qy	301	LGHNTASIML	FGGAVSEVSNGTSSRRAGCVWLLPLLVHLLKX	344
Db	301	LGHNTASIML	FGGAVSEVSNGTSSRRAGCVWLLPLLVHLLKX	344

US-09-999-833A-523
; Sequence 523, Application US/09999833A
; Patent No. 6916648
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918595
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29

```

; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match      i 100.0%; Score 1806; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-172;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTIQPKWNNISWAIETGLAALCLFQGVPRSGDATFPKAMDNVTVRQESATLRCTID 60
    |||||
Db 1 MKTIQPKWNNISWAIETGLAALCLFQGVPRSGDATFPKAMDNVTVRQESATLRCTID 60
    |||||

Qy 61 NRVTVAWLNRSTILYAGNDKWCIDPRVLLSNTQTQYSIEIQNDVYDEGPYTCVSQTD 120
    |||||
Db 61 NRVTVAWLNRSTILYAGNDKWCIDPRVLLSNTQTQYSIEIQNDVYDEGPYTCVSQTD 120
    |||||

Qy 121 NHPKTSRVHLIVQSPKIVISSDINSIGNNLSLTCTATGRPEPTVWRHISPKAVGFV 180
    |||||
Db 121 NHPKTSRVHLIVQSPKIVISSDINSIGNNLSLTCTATGRPEPTVWRHISPKAVGFV 180
    |||||

Qy 181 SEDEYLEIQGITREQSGDYECASNDVAAPVVRVKVTYVNPYISEAKGTGVPVGQGT 240
    |||||
```

```

Db 181 SEDEYLEIQGITREQSGDYECASNDVAAPVVRVKVTYVNPYISEAKGTGVPVGQGT 240
    |||||
Qy 241 LOCEASAVPSAEFQYKDDKRLIEGKKGKVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
    |||||
Db 241 LOCEASAVPSAEFQYKDDKRLIEGKKGKVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
    |||||
Qy 301 LGHTNASIMLFGPGAVSEVSNGTSSRAGCVWLLPLLLVHLHLKPF 344
    |||||
Db 301 LGHTNASIMLFGPGAVSEVSNGTSSRAGCVWLLPLLLVHLHLKPF 344
    |||||

RESULT 3
US-10-020-445A-523
; Sequence 523, Application US/10020445A
; Patent No. 6962797
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC74
; CURRENT APPLICATION NUMBER: US/10/020,445A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
```

; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797

; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1806; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-172;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKMNSISWALFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
DB 1 MKTIQPKMNSISWALFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTID 60
QY 61 NRTRVAVLNRSITLYAGNDKWCIDPRVLLSNTQYTSIEIQNVVDYDEGPTCSVQTD 120
DB 61 NRTRVAVLNRSITLYAGNDKWCIDPRVLLSNTQYTSIEIQNVVDYDEGPTCSVQTD 120
QY 121 NHPKTSRVHLIVQVSPKIVEISSDINSGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
DB 121 NHPKTSRVHLIVQVSPKIVEISSDINSGNNISLTCIATGRPEPTVTRHISPKAVGFV 180
QY 181 SEDEYLEIQITREQSGDYSCSASNDVAAPVRRVKVTNNYPPIYISEAKGTGVPVQKGT 240
DB 181 SEDEYLEIQITREQSGDYSCSASNDVAAPVRRVKVTNNYPPIYISEAKGTGVPVQKGT 240
QY 241 LOCEASAVPSAEQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
DB 241 LOCEASAVPSAEQWYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
QY 301 LGHTNASIMLFGCAVSEVSNGTSSRRAGCVWLLPLVLHLLKF 344
DB 301 LGHTNASIMLFGCAVSEVSNGTSSRRAGCVWLLPLVLHLLKF 344
RESULT 4
US-09-700-397-4
; Sequence 4, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JF99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-700-397-4
Query Match 90.9%; Score 1642; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 6.8e-156;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 RSGDATFPKAMDNVTVRQGESATLRCTIDNRTRVAVLNRSITLYAGNDKWCIDPRVLL 91
DB 1 RSGDATFPKAMDNVTVRQGESATLRCTIDNRTRVAVLNRSITLYAGNDKWCIDPRVLL 60
QY 92 SNTQYTSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDINSGN 151
DB 61 SNTQYTSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDINSGN 120
QY 152 NISLTCIATGRPEPTVTRHISPKAVGFSEDEYLEIQITREQSGDYSCSASNDVAAPV 211
DB 121 NISLTCIATGRPEPTVTRHISPKAVGFSEDEYLEIQITREQSGDYSCSASNDVAAPV 180
QY 212 VRRVKVTNNYPPIYISEAKGTGVPVQKGTQCEASAVPSAEFQWKDKRLIEGKGVK 271
DB 181 VRRVKVTNNYPPIYISEAKGTGVPVQKGTQCEASAVPSAEFQWKDKRLIEGKGVK 240
QY 272 ENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGCAVSEVSNGTSSRRAGCVW 331
DB 241 ENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGCAVSEVSNGTSSRRAGCVW 300
QY 332 LLPLVLHLLKF 344
|||||

DB 301 LLPLVLHLLKF 313
RESULT 5
US-09-976-594-404
; Sequence 404, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 404
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CD1
US-09-976-594-404
Query Match 51.6%; Score 931.5; DB 2; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.1e-84;
Matches 180; Conservative 60; Mismatches 80; Indels 5; Gaps 4;
QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRTRVAVLNRSITLYAG 78
DB 17 LRLLCLLPTGLPVRSD--FNRGTDNITVRQGDALLRCVLEDKNGKVAWLNRSIGIFAG 74
QY 79 NDKWCLDPRVLLSNTQYTSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLDPRVELEKHSLEYSLRIOKVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 134
QY 139 VEISSDINSGNNISLTCIATGRPEPTVTRHISPKAVGFSEDEYLEIQITREQSGD 198
DB 135 SNISSDVTVEGNSVTLVCWANGRPEPVITWRHLTPTGREFEGESEYLEITGITREQSGK 194
QY 199 YECASANDVAAPVRRVKVTNNYPPIYISEAKGTGVPVQKGTQCEASAVPSAEFQWKD 258
DB 195 YECCAANEVSSADVQKVTVNYPPTITESKNEATGTGQASLKCEASAVPDPFEWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGCAVSE 318
DB 255 DTR-INSANGLEIKSTEGQSSLTVTNVTTEHYGNYTCVAANKLGVTNASLVLPFGSVRG 313
QY 319 VSGTSSRRAGCVWLLPLVLHLLK 343
DB 314 I-NGSISLAVPLWLLAASLLCLLSK 337
RESULT 6
US-08-414-657D-42
; Sequence 42, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ

```
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-42

Query Match 51.3%; Score 926.5; DB 1; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMNVTVRQGESATLRCTIDNRVTRVLAWLNRSTLYAG 78
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTALRCVVDKSKVLAWLNRSGIIFAG 74

QY 79 NDKWCLDRPVLLSNTQTOYSIEIQNVVYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDRPVELEKHALEYSRIQKVDVYDEGPTCSVQTOHEPKTSQVYLIVQVPPKI 134

QY 139 VEISDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
Db 135 SNISSDVTNVEGNNVTLVCMANGREPEVTWRHLTPLGREFEGEEYLEILGITREQSGK 194

QY 199 YECASNDVAAPVRRVKVTNYPPIYISBAKGTGVPVGOKGTLOCEASAVPSAEFOWYKD 258
Db 195 YECCAANEVSSADVQVKVTNYPPTITESKSNEATTGQASLKCEASAVPAPDFEYRD 254

QY 259 DXRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTTEEYGNVTCVAANKLGVTNASLVLFRPGSVRG 313

QY 319 VSGTSRRAGCVWLLPLVHLHLK 343
Db 314 I-NGSISLAVPLMLLAASLFCLLSK 337
```

```
RESULT 7
US-08-414-657D-43
; Sequence 43, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
```

```
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-43
```

```
Query Match 51.3%; Score 926.5; DB 1; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMNVTVRQGESATLRCTIDNRVTRVLAWLNRSTLYAG 78
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTALRCVVDKSKVLAWLNRSGIIFAG 74

QY 79 NDKWCLDRPVLLSNTQTOYSIEIQNVVYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDRPVELEKHALEYSRIQKVDVYDEGPTCSVQTOHEPKTSQVYLIVQVPPKI 134

QY 139 VEISDISINEGNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREQSGD 198
Db 135 SNISSDVTNVEGNNVTLVCMANGREPEVTWRHLTPLGREFEGEEYLEILGITREQSGK 194

QY 199 YECASNDVAAPVRRVKVTNYPPIYISBAKGTGVPVGOKGTLOCEASAVPSAEFOWYKD 258
Db 195 YECCAANEVSSADVQVKVTNYPPTITESKSNEATTGQASLKCEASAVPAPDFEYRD 254

QY 259 DXRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTTEEYGNVTCVAANKLGVTNASLVLFRPGSVRG 313

QY 319 VSGTSRRAGCVWLLPLVHLHLK 343
Db 314 I-NGSISLAVPLMLLAASLFCLLSK 337
```

```
RESULT 8
US-09-135-080-4
; Sequence 4, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
```

```

;
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-135-080-4

```

```

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

Qy 20 LAALCLF-QGVPRSGDATPPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSITLYAG 78
Db 17 LRLCLLPTGLPVRSVD--FNRGTDNITVRQGDITAILRCVVEDKNSKVAVLNRSIGIFAG 74

Qy 79 NDKWCLDPRVLLSNTQTOYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDPRVLEKRHALEYSLRIQKVDVDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 134

Qy 139 VEISSDISINEGNNISLTCTIATGRPEPTVTRHISPKAVGVSEDEYLEIQGITREOSGD 198
Db 135 SNISSDVTNVEGNNVTLVCMANGRPVITWRHLTPGRFEGEEVEYLEILGITREOSGK 194

Qy 199 YECASANDVAAPVRRVKVTNYPPISEAKGTGVPVGQKGTLOCEASAVPSAEFOWYKD 258
Db 195 YECCAANEVSSADVKQVKVTNYPPTITESKNEATTGRQASLKCEASAVPAPDFEYRD 254

Qy 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTTEHYGNYTCVAANKLGVNTNASLVLFRPGSVRG 313

Qy 319 VNGTSRRAGCVWLLPLLLHLK 343
Db 314 I-NGSISLAVPLWLLAASLFCLLSK 337

```

```

RESULT 9
US-08-414-657D-2
; Sequence 2, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak

```

```

; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-414-657D-2

```

```

Query Match 51.1%; Score 923.5; DB 1; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

Qy 20 LAALCLF-QGVPRSGDATPPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSITLYAG 78
Db 10 LRLCLLPTGLPVRSVD--FNRGTDNITVRQGDITAILRCVLEDKNSKVAVLNRSIGIFAG 67

Qy 79 NDKWCLDPRVLLSNTQTOYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 68 HDKWSLDPRVLEKRHALEYSLRIQKVDVDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127

Qy 139 VEISSDISINEGNNISLTCTIATGRPEPTVTRHISPKAVGVSEDEYLEIQGITREOSGD 198
Db 128 SNISSDVTNVEGNNVTLVCMANGRPVITWRHLTPGRFEGEEVEYLEILGITREOSGK 187

Qy 199 YECASANDVAAPVRRVKVTNYPPISEAKGTGVPVGQKGTLOCEASAVPSAEFOWYKD 258
Db 188 YECCAANEVSSADVKQVKVTNYPPTITESKNEATTGRQASLKCEASAVPAPDFEYRD 247

Qy 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTNASIMLFGPGAVSE 318
Db 248 DTR-INSANGLEIKSTEGQSSLTVTNVTTEHYGNYTCVAANKLGVNTNASLVLFRPGSVRG 306

Qy 319 VNGTSRRAGCVWLLPLLLVL 338
Db 307 I-NGSISLAVPLWLLAASLL 325

```

```

RESULT 10
US-08-414-657D-41
; Sequence 41, Application US/08414657D

```

```
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-41

Query Match 51.1%; Score 923.5; DB 1; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
Db 10 LRLLCLLPTGLPVRSD--FNRGTDNITVRQGDITAILRCVLEDKNSKVAWLNRSGIIFAG 67
QY 79 NDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 68 HDKWSLDPRVLEKHSLEYSLRIOKVVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
QY 139 VEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREOSGD 198
Db 128 SNISSDVTNEGSNTLVCMANGRPEPTVTRHLLTPTGREFEGBEYLEILGITREOSGK 187
QY 199 YECASNDVAAPVVRVKVTNNYPVYISEAKGTGVPVGQKGTLOCEASAVPSAEFOWYKD 258
Db 188 YECKAANEVSSADVQKVTVNYPPTITESKSNNEATTGQASLKCEASAVPAPDFEYRD 247
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
Db 248 DTR-INSANGLEIKSTEGQSSLTVTNTEEHYGNVTCVAANKLGVTNASLVLFRPGSVRG 306
QY 319 VNGTSRRAGCVWLLPLVL 338
Db 307 I-NGSISLAVPLWLLAALL 325
```

```
RESULT 11
US-09-135-080-2
; Sequence 2, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-135-080-2
```

```
Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYAG 78
Db 10 LRLLCLLPTGLPVRSD--FNRGTDNITVRQGDITAILRCVLEDKNSKVAWLNRSGIIFAG 67
QY 79 NDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 68 HDKWSLDPRVLEKHSLEYSLRIOKVVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
QY 139 VEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREOSGD 198
Db 128 SNISSDVTNEGSNTLVCMANGRPEPTVTRHLLTPTGREFEGBEYLEILGITREOSGK 187
QY 199 YECASNDVAAPVVRVKVTNNYPVYISEAKGTGVPVGQKGTLOCEASAVPSAEFOWYKD 258
Db 188 YECKAANEVSSADVQKVTVNYPPTITESKSNNEATTGQASLKCEASAVPAPDFEYRD 247
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
Db 248 DTR-INSANGLEIKSTEGQSSLTVTNTEEHYGNVTCVAANKLGVTNASLVLFRPGSVRG 306
```


Qy	319	V	S	N	G	T	S	?	R	A	G	C	V	W	L	L	P	L	L	V	338
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
Db	307	I	-	N	G	S	I	S	L	A	V	P	L	W	L	L	A	A	S	L	325

RESULT 12

```

US-08-414-657D-60
; Sequence 60, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukarska, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-414-657D-60

```

Query Match	51.1%	Score 923.5	DB 1	Length 338
Best Local Similarity	55.1%	Pred. No. 7.2e-84		
Matches 179	Conservative	60	Mismatches 81	Indels 5
Gaps				
Qy	20	LAALCLF-QGVPRSGDATFPKAMDNVTVRQESATLRCTIDNRVTRVAMLNRSITLIYAG	78	
Db	17	LRLCLLPTGLPVESVD--FNRGTDNITVRQDITAILRCVLEDKSKVAMLNRSIIIFAG	74	
Qy	79	NKKWCLDPRVLLSNTQTQYSIEITQNVVDYDEGPTCTSVQTDNHPKTSRVHLIIIVQSPKI	138	
Db	75	HDKWSLDPRVELEKHSLEYSLSRLOKVDVYDEGYSYTSVQTHPEKTSQVYLIIVQVPPI	134	
Qy	139	VEISSDTSINEGNNISLTCTATGRPEPTVTVRRHSIPKAVGFSVDEYLEIOGIREOSGD	198	
Db	135	SNISSDVTVEGNSVTLVCMANGREPPIVTVRRHTPTGREPEGEVEYLEILGITREQSGK	194	
Qy	199	YECASANDVAAVTVRRVKVTVNYPPYISEAKGTGPVQOKTLOCEASAVPSAFOWYKD	258	
Db	195	YECKAAVEVSADYQVKVTVNYPPYITETESKNEATTGROASLKCEASAVPAPOFEWYRD	254	
Qy	259	DKRLIEGKGGVKVBNRNPFLSKLIIPFNVSEHDYGNVTCVASNKLGHNTASIMLPFGAVSE	318	

255 DTR -INSANGLEIKSTEGQS^{LT}VTWYTEEHGYNT^{CV}AA^{NG}KL^{GT}NA^{SL}VL^{PR}GS^{VRG} 313

319 VSNGTS^RBAGC^WLL^{PL}LV^LHL^LLK 343

314 I-NGSIS^{LA}VP^{LI}WL^{LA}AS^{LL}CL^{LS}K 337

RESULT 13

```

RESULT 13
US-09-135-080-8
; Sequence 8, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimental, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-135-080-8

```

	Query Match	51.1%	Score 923.5	DB 2	Length 338
	Best Local Similarity	55.1%	Pred. No. 7.2e-84		
	Matches 179	Conservative	60	Mismatches 81	Indels 5
					Gaps 4
Qy	20	LAALCLF-QGVPRSGDATFPKAMDVTVVRQGESATLRCTIDNRVTRVAVLNRSTILYAG	78		
Db	17	LRELCLLPTGLPVRSD--FNRTGDNITVRQGGTAILRCVLDEKNSKVAVLNRSGIIFAG	74		
Qy	79	NDKWLCDLPRVVLNSLTQTVSISIQNVVDVDEGPTVCSVQTDNHPKTSRVLHLVQVSPKI	138		
Db	75	HDKWLSDPRVLEKRLSLEYSLRIQKVDVDEGTSVCSVQTHPEKPTSVYVLIVQVPKI	134		
Qy	139	VEISSDISINEGNISILCTIATCRPPVTVWRIISPKAVGVSEDEVLETQGITRQSGD	198		
Db	135	SNITSSDVTVNEGSNVLIVCMANGRPVITWRHLITPTGTFEGEGBEYLEILGITRQSGK	194		
Qy	199	YECSASNDVAAPVVRVKKVTVNVYPPYISEAKGTGTVPGQKGTLOCRASAVPSAEFOWYKD	258		

Db 195 YECCAANEVSSADVQVKVTVNYPPTITESKSNKNEATTGROASLKCEASAVPAPDFEYRD 254
 QY 259 DXELIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIMLFGPGAVSE 318
 Db 255 DTR-INSANGLEIKSTEGOSSLTVTWVBTEBHYGNYTCVAAANKLGVTNASLVLFRPGSVRG 313
 QY 319 VSGTSTRACGVWLLPLLLVHLHLK 343
 Db 314 I-NGSISLAVPLWLLAASLLCLLSK 337

RESULT 14
 US-08-414-657D-46
 ; Sequence 46, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 46:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-414-657D-46

Query Match 50.3%; Score 908; DB 1; Length 308;
 Best Local Similarity 56.3%; Pred. No. 2.2e-82;
 Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;
 QY 20 LAALCLF-QGVPRSGDTPPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
 Db 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQGDTAILRCVLEDKSKVAVLNRSGIIFAG 67
 QY 79 NDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
 Db 68 HDKWSLDPRLVEKRHSLEYSRLRIQKVDVYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
 QY 139 VEISSDISINEGNISLTICATGRPEPTVTRHISPKAVGFVSEDEYLETQGITREQSGD 198
 Db 128 SNISSDVTNVEGNSVTLVCMANGRPVITWRHLITPTGREFEGBEYLETILGITREQSGK 187

QY 199 YECASNDVAAPVRRVKVTVNYPVISAQKGTGVPVGKGTLOCEASAVPSAEFOWYKD 258
 Db 188 YECCAANEVSSADVQVKVTVNYPPTITESKSNKNEATTGROASLKCEASAVPAPDFEYRD 247
 QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIMLFGPGAVSE 318
 Db 248 DTR-INSANGLEIKSTEGOSSLTVTWVBTEBHYGNYTCVAAANKLGVTNASLVLFRPGSVRG 306
 QY 319 VS 320
 ;
 Db 307 IN 308
 RESULT 15
 US-08-414-657D-47
 ; Sequence 47, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 47:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 315 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-414-657D-47

Query Match 50.2%; Score 907; DB 1; Length 315;
 Best Local Similarity 56.3%; Pred. No. 2.9e-82;
 Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;
 QY 20 LAALCLF-QGVPRSGDTPPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
 Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQGDTAILRCVLEDKSKVAVLNRSGIIFAG 74
 QY 79 NDKWCLDPRVLLSNTQTQYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
 Db 75 HDKWSLDPRLVEKRHSLEYSRLRIQKVDVYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 134

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.
OM protein - protein search, using sw model.
Run on: February 15, 2006, 02:02:26 ; Search time 163 Seconds
(without alignments)
881.799 Million cell updates/sec
Perfect score: 1806;
Sequence: 1 MKTIQPMKMSISWAIFTGL.....RRAGCVMLDPLLVHLLKFP 344
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
52	1806	100.0	344	4	US-10-066-269-104
64	1806	100.0	344	4	US-10-167-749-523
226	1806	100.0	344	4	US-10-223-085-56
232	1806	100.0	344	4	US-10-219-065-126
262	1806	100.0	344	4	US-10-223-084-56
263	1806	100.0	344	4	US-10-223-088-56
264	1806	100.0	344	4	US-10-223-090-56
269	1806	100.0	344	4	US-10-223-087-56
271	1806	100.0	344	4	US-10-223-083-56
474	1806	100.0	344	4	US-10-223-089-56
274	1806	100.0	344	4	US-10-223-081-56
485	1806	100.0	344	4	US-10-223-082-56
554	1806	100.0	344	4	US-10-170-481A-523
556	1806	100.0	344	4	US-10-210-028-523
615	1806	100.0	344	4	US-10-162-521A-523
623	1806	100.0	344	4	US-10-305-654-56
635	1806	100.0	344	4	US-10-657-103-3
639	1806	100.0	344	4	US-10-081-056-56
659	1806	100.0	344	5	US-10-918-851-523
660	1806	100.0	344	5	US-10-931-886-376
661	1806	100.0	344	5	US-10-805-667-523
662	1806	100.0	344	5	US-10-897-359-523
664	1806	100.0	344	5	US-10-893-802-523
665	1806	100.0	344	5	US-10-897-360-523
666	1806	100.0	344	5	US-10-955-952-376
668	1806	100.0	344	6	US-11-129-762-523
669	1799	99.6	344	3	US-09-966-546-4
670	1799	99.6	344	3	US-09-966-546-6

671	1799	99.6	344	3	US-09-966-545-4	Sequence 4, Appli
672	1799	99.6	344	3	US-09-966-545-6	Sequence 6, Appli
673	1799	99.6	344	3	US-09-965-212-4	Sequence 4, Appli
674	1799	99.6	344	3	US-09-965-212-6	Sequence 6, Appli
675	1799	99.6	344	4	US-10-189-940-4	Sequence 4, Appli
676	1799	99.6	344	4	US-10-189-940-6	Sequence 6, Appli
677	1799	99.6	344	5	US-10-971-479-4	Sequence 6, Appli
678	1799	99.6	344	5	US-10-971-479-6	Sequence 6, Appli
679	1665.5	92.2	344	4	US-10-161-572-50	Sequence 456, App
680	1665.5	92.2	344	4	US-10-295-027-456	Sequence 456, App
681	1650	91.4	355	4	US-10-306-133-1	Sequence 1, Appli
682	1642	90.9	313	4	US-10-657-103-4	Sequence 4, Appli
683	1639.5	90.8	344	4	US-10-306-133-3	Sequence 3, Appli
684	1427.5	79.0	344	4	US-10-015-115-87	Sequence 87, Appl
685	1295	71.7	250	4	US-10-311-823-15	Sequence 15, Appl
686	1285.5	71.2	338	4	US-10-015-115-86	Sequence 86, Appl
687	1268	70.2	345	4	US-10-161-572-59	Sequence 59, Appl
688	1268	70.2	345	4	US-10-015-115-84	Sequence 84, Appl
689	1268	70.2	345	5	US-10-696-639-46	Sequence 46, Appl
690	1266	70.1	345	4	US-10-015-115-83	Sequence 83, Appl
691	1259	69.7	345	4	US-10-015-115-85	Sequence 85, Appl
692	938.5	52.0	338	4	US-10-038-854-159	Sequence 159, App
693	931.5	51.6	338	3	US-09-808-602-69	Sequence 69, Appl
694	931.5	51.6	338	3	US-09-800-198-58	Sequence 58, Appl
696	931.5	51.6	338	4	US-10-161-572-58	Sequence 58, Appl
697	931.5	51.6	338	4	US-10-038-854-158	Sequence 158, App
698	930.5	51.5	350	3	US-10-042-865-92	Sequence 92, Appl
699	930.5	51.5	350	3	US-09-808-602-71	Sequence 71, Appl
700	926.5	51.3	338	3	US-09-800-198-60	Sequence 60, Appl
701	926.5	51.3	338	3	US-09-808-602-72	Sequence 72, Appl
702	926.5	51.3	338	3	US-09-800-198-61	Sequence 61, Appl
703	893	49.4	333	4	US-10-042-865-91	Sequence 91, Appl
704	893	49.4	333	5	US-09-978-418-38	Sequence 38, Appl
705	873.5	48.4	203	4	US-10-485-231-38	Sequence 38, Appl
706	852.5	47.2	326	4	US-10-187-975-108	Sequence 108, App
707	842	46.6	352	4	US-10-106-698-5794	Sequence 5794, App
708	842	46.6	352	4	US-10-038-854-156	Sequence 156, App
715	823	45.6	354	4	US-10-042-865-89	Sequence 89, Appl
763	823	45.6	354	4	US-10-066-269-130	Sequence 130, App
819	823	45.6	354	4	US-10-219-065-2	Sequence 2, Appli
822	823	45.6	354	4	US-10-038-854-24	Sequence 24, Appl
825	822	45.4	354	4	US-10-312-352-15	Sequence 15, Appl
826	822	45.4	354	4	US-10-042-865-14	Sequence 14, Appl
827	819	45.3	354	4	US-10-104-047-2965	Sequence 2965, Ap
828	815	45.1	348	4	US-10-038-854-26	Sequence 26, Appl
829	815	45.1	348	4	US-10-161-572-56	Sequence 56, Appl
830	815	45.1	348	4	US-10-161-572-57	Sequence 57, Appl
831	815	45.1	348	4	US-10-038-854-155	Sequence 155, App
866	815	45.1	348	4	US-10-042-865-88	Sequence 88, Appl
902	815	45.1	352	4	US-10-167-749-612	Sequence 612, App
904	815	45.1	352	4	US-10-170-481A-612	Sequence 612, App
909	815	45.1	352	4	US-10-210-028-612	Sequence 612, App
921	815	45.1	352	5	US-10-162-521A-612	Sequence 612, App
922	815	45.1	352	5	US-10-918-851-612	Sequence 612, App
923	815	45.1	352	5	US-10-805-667-612	Sequence 612, App
924	815	45.1	352	5	US-10-897-359-612	Sequence 612, App
925	815	45.1	352	5	US-10-893-802-612	Sequence 612, App
927	815	45.1	352	6	US-10-897-360-612	Sequence 612, App
928	815	45.1	352	6	US-11-129-762-612	Sequence 612, App
929	763	42.2	336	4	US-10-471-449-9	Sequence 9, Appli
930	761	42.1	319	4	US-10-480-172-8	Sequence 22, Appl
931	761	42.1	319	4	US-10-015-115-22	Sequence 24, Appl
932	757	41.9	307	4	US-10-015-115-26	Sequence 26, Appl
933	726	40.2	336	4	US-10-332-947-53	Sequence 53, Appl
934	721	39.9	336	4	US-10-015-115-28	Sequence 28, Appl
935	720.5	39.9	281	3	US-09-764-853-561	Sequence 561, App
936	681.5	37.7	351	4	US-10-332-947-52	Sequence 52, Appl
937	632	35.0	133	4	US-10-378-029-73	Sequence 73, Appl
938	603	33.4	141	5	US-10-450-763-44207	Sequence 44207, A
939	599	33.2	261	4	US-10-038-854-157	Sequence 157, App
940	599	33.2	261	4	US-11-129-762-523	Sequence 90, Appl
941	569.5	31.5	130	5	US-10-042-865-90	Sequence 44206, A

942	527	29.2	256	4	US-10-480-172-14	Sequence 14, Appl	1015	253.5	14.0	404	3	US-09-977-418-24	Sequence 24, Appl
943	525.5	29.1	872	5	US-10-450-763-44175	Sequence 44175, A	1016	253.5	14.0	404	3	US-09-977-033A-24	Sequence 24, Appl
944	472	26.1	241	4	US-10-480-172-12	Sequence 12, Appl	1017	253.5	14.0	404	3	US-09-977-751C-24	Sequence 24, Appl
945	338.5	18.7	413	6	US-11-097-143-35247	Sequence 35247, A	1018	253.5	14.0	404	3	US-09-977-639A-24	Sequence 24, Appl
946	333	18.4	315	6	US-11-097-143-23718	Sequence 23718, A	1019	253.5	14.0	404	3	US-09-977-819B-24	Sequence 24, Appl
947	308.5	17.1	528	4	US-10-108-605-49	Sequence 49, Appl	1020	253.5	14.0	404	4	US-10-161-572-44	Sequence 44, Appl
948	306	16.9	545	6	US-11-097-143-14514	Sequence 14514, A	1021	253	14.0	570	4	US-10-311-823-13	Sequence 13, Appl
949	297.5	16.5	333	6	US-11-097-143-3633	Sequence 3633, Ap	1022	253	14.0	586	4	US-10-311-823-7	Sequence 7, Appl
950	290.5	16.1	2572	4	US-10-114-153-86	Sequence 86, Appl	1023	250.5	13.9	885	6	US-11-097-143-11298	Sequence 11298, A
951	290.5	16.1	2673	4	US-10-120-801-76	Sequence 76, Appl	1024	250	13.8	374	4	US-10-311-823-16	Sequence 16, Appl
952	290.5	16.1	2673	5	US-10-934-998-101	Sequence 101, App	1025	250	13.8	442	4	US-10-311-823-12	Sequence 12, Appl
953	290.5	16.1	4495	4	US-10-138-588-20	Sequence 20, Appl	1026	250	13.8	458	4	US-10-311-823-4	Sequence 4, Appl
954	290.5	16.1	5636	4	US-10-032-189-128	Sequence 128, App	1027	250	13.8	1219	5	US-10-450-763-42459	Sequence 42459, A
955	290.5	16.1	5636	4	US-10-120-801-72	Sequence 72, Appl	1028	250	13.8	1315	4	US-10-094-886-52	Sequence 52, Appl
956	290.5	16.1	5636	4	US-10-023-634-93	Sequence 93, Appl	1029	250	13.8	1386	4	US-10-094-886-38	Sequence 38, Appl
957	290.5	16.1	5636	4	US-10-408-765A-1895	Sequence 1895, Ap	1030	249.5	13.8	607	3	US-09-991-326-12	Sequence 12, Appl
958	290.5	16.1	5636	5	US-10-934-998-81	Sequence 81, Appl	1031	249.5	13.8	1040	4	US-10-712-124-10	Sequence 10, Appl
959	288.5	16.0	707	4	US-10-138-588-18	Sequence 18, Appl	1032	248	13.7	467	6	US-11-097-143-33438	Sequence 33438, A
960	288.5	16.0	961	4	US-10-162-335-42	Sequence 42, Appl	1033	246.5	13.6	1007	4	US-10-408-765A-118	Sequence 118, App
961	288.5	16.0	1240	5	US-10-450-763-34292	Sequence 34292, A	1034	246.5	13.6	1018	4	US-10-367-978-67	Sequence 67, Appl
962	288.5	16.0	1336	4	US-10-450-763-34292	Sequence 33, Appl	1035	246.5	13.6	1018	4	US-10-712-124-88	Sequence 88, Appl
963	288.5	16.0	1902	4	US-10-019-065A-33	Sequence 33, Appl	1036	246.5	13.6	1018	5	US-10-631-467-948	Sequence 948, App
964	288.5	16.0	1953	4	US-10-114-153-88	Sequence 88, Appl	1037	244.5	13.5	512	4	US-10-631-467-948	Sequence 2493, Ap
965	288.5	16.0	1953	4	US-10-115-479-88	Sequence 88, Appl	1037	244.5	13.5	512	4	US-10-094-749-2493	Sequence 2493, Ap
966	288.5	16.0	3645	4	US-10-1032-189-127	Sequence 127, App	1038	243.5	13.5	605	3	US-09-991-326-8	Sequence 8, Appl
967	288.5	16.0	3645	4	US-10-120-801-73	Sequence 73, Appl	1039	242.5	13.4	792	5	US-10-450-763-33418	Sequence 33418, A
968	288.5	16.0	4126	6	US-11-049-637-4	Sequence 4, Appl	1040	242.5	13.4	893	5	US-10-450-763-30617	Sequence 30617, A
969	288.5	16.0	5518	6	US-11-049-637-2	Sequence 2, Appl	1041	242.5	13.4	893	5	US-10-450-763-30970	Sequence 30970, A
970	288.5	16.0	5622	5	US-10-773-446-128	Sequence 128, App	1042	242	13.4	2586	3	US-09-729-485A-11	Sequence 11, Appl
971	288.5	16.0	5635	4	US-10-451-168-78	Sequence 78, App	1043	242	13.4	2586	3	US-09-729-485A-14	Sequence 14, Appl
972	288.5	16.0	5635	5	US-10-980-387-78	Sequence 78, Appl	1044	242	13.4	2586	3	US-09-802-318-11	Sequence 11, Appl
973	284.5	15.8	467	6	US-11-097-143-1524	Sequence 1524, A	1045	242	13.4	2586	3	US-09-802-318-14	Sequence 14, Appl
974	276	15.3	733	4	US-10-023-634-92	Sequence 92, Appl	1046	242	13.4	2586	3	US-09-905-129-11	Sequence 11, Appl
975	276	15.3	848	4	US-10-094-749-3192	Sequence 3192, Ap	1047	242	13.4	2586	3	US-09-905-129-14	Sequence 14, Appl
976	276	15.3	848	4	US-10-311-509-21	Sequence 21, Appl	1048	242	13.4	2586	3	US-09-991-630-11	Sequence 11, Appl
977	276	15.3	848	5	US-10-482-029-204	Sequence 204, App	1049	242	13.4	2586	3	US-09-991-630-14	Sequence 14, Appl
978	276	15.3	848	5	US-10-852-335A-113	Sequence 113, App	1050	242	13.4	2586	4	US-10-454-351-11	Sequence 11, Appl
979	275.5	15.3	853	5	US-10-992-287-48	Sequence 48, Appl	1051	242	13.4	2586	4	US-10-454-351-14	Sequence 14, Appl
980	275	15.2	848	4	US-10-496-905-513	Sequence 513, App	1052	242	13.4	2587	3	US-09-729-485A-16	Sequence 16, Appl
981	274	15.2	1477	4	US-10-207-655-180	Sequence 180, App	1053	242	13.4	2587	3	US-09-802-318-16	Sequence 16, Appl
982	273.5	15.1	1356	4	US-10-274-583-20	Sequence 20, Appl	1054	242	13.4	2587	3	US-09-905-129-16	Sequence 16, Appl
983	271.5	15.0	1426	4	US-10-085-198-108	Sequence 108, App	1055	242	13.4	2587	3	US-09-991-630-16	Sequence 16, Appl
984	270	15.0	1426	4	US-10-085-198-106	Sequence 106, App	1056	242	13.4	2587	4	US-10-454-351-16	Sequence 16, Appl
985	269	14.9	152	4	US-10-085-198-106	Sequence 106, App	1057	242	13.4	2589	3	US-09-991-630-24	Sequence 24, Appl
986	268.5	14.9	1479	4	US-11-097-143-32490	Sequence 32490, A	1058	242	13.4	2589	4	US-10-454-351-24	Sequence 24, Appl
987	268.5	14.9	1496	4	US-10-091-438-168	Sequence 168, App	1059	241.5	13.4	1020	5	US-10-631-467-1637	Sequence 1637, Ap
988	268.5	14.9	1496	4	US-10-231-956A-325	Sequence 325, App	1060	241	13.3	891	5	US-10-450-763-37895	Sequence 37895, A
989	268.5	14.9	1496	4	US-10-021-660-125	Sequence 125, App	1061	240	13.3	3707	5	US-10-852-335A-139	Sequence 139, App
990	268.5	14.9	1496	4	US-10-331-496A-28	Sequence 28, Appl	1062	238.5	13.2	1024	5	US-10-737-318-41	Sequence 41, Appl
991	268.5	14.9	1496	5	US-10-211-462-87	Sequence 87, Appl	1063	235.5	13.0	2623	4	US-10-454-351-32	Sequence 32, Appl
992	268.5	14.9	1496	5	US-10-723-860-1721	Sequence 1721, Ap	1064	235	13.0	662	4	US-10-369-493-6726	Sequence 6726, Ap
993	268.5	14.9	1496	5	US-10-496-905-616	Sequence 616, App	1065	235	13.0	662	4	US-10-369-493-6344	Sequence 6344, Ap
994	268.5	14.9	1496	5	US-10-745-237-344	Sequence 344, App	1066	232.5	12.9	2783	4	US-10-369-493-6344	Sequence 6344, Ap
995	268.5	14.9	1496	5	US-10-745-237-350	Sequence 350, App	1066	232	12.8	2591	4	US-10-032-189-56	Sequence 56, Appl
996	268.5	14.9	1498	4	US-10-745-237-350	Sequence 350, App	1067	232	12.8	2617	4	US-10-032-189-46	Sequence 46, Appl
997	266	14.7	36946	5	US-10-243-552-899	Sequence 899, App	1068	232	12.8	3911	4	US-10-032-189-46	Sequence 46, Appl
998	261	14.5	1395	3	US-10-840-512-155	Sequence 155, App	1069	230.5	12.8	868	4	US-10-032-189-46	Sequence 46, Appl
999	261	14.5	1395	3	US-09-808-602-67	Sequence 67, Appl	1070	230	12.7	4393	4	US-10-016-283-1	Sequence 1, Appl
1000	261	14.5	1395	3	US-09-800-198-56	Sequence 56, Appl	1071	230	12.7	4393	5	US-10-741-600-1105	Sequence 1105, Ap
1001	261	14.5	1395	4	US-10-289-776-15	Sequence 15, Appl	1072	230	12.7	4436	5	US-10-450-763-53624	Sequence 53624, A
1002	261	14.5	1395	5	US-10-826-812-2	Sequence 2, Appl	1073	229.5	12.7	849	4	US-10-435-751-161	Sequence 161, App
1003	260.5	14.4	496	6	US-11-022-546-15	Sequence 15, Appl	1074	229.5	12.7	851	4	US-10-435-751-162	Sequence 162, Appl
1004	260	14.4	1395	6	US-11-097-143-12948	Sequence 12948, A	1075	229.5	12.7	869	4	US-10-016-283-33	Sequence 33, Appl
1005	259	14.3	34350	5	US-11-097-143-31563	Sequence 31563, A	1076	229.5	12.7	869	5	US-10-745-237-274	Sequence 274, App
1006	259	14.3	34350	5	US-10-745-237-394	Sequence 394, App	1077	229.5	12.7	893	4	US-10-435-751-7	Sequence 7, Appl
1007	255.5	14.1	1024	5	US-10-737-318-44	Sequence 44, Appl	1078	229.5	12.7	893	4	US-10-435-751-22	Sequence 22, Appl
1008	255.5	14.1	1024	6	US-10-737-318-46	Sequence 46, Appl	1079	229.5	12.7	893	4	US-10-435-751-160	Sequence 160, App
1009	255	14.1	359	6	US-11-097-143-18552	Sequence 18552, A	1080	229.5	12.7	893	4	US-10-435-751-201	Sequence 201, App
1010	254.5	14.1	5175	4	US-10-120-801-74	Sequence 74, Appl	1081	229.5	12.7	1117	4	US-10-435-751-9	Sequence 9, Appl
1011	254.5	14.1	5175	4	US-10-369-493-6859	Sequence 6859, Ap	1082	229.5	12.7	1117	4	US-10-435-751-23	Sequence 23, Appl
1012	254.5	14.1	5175	4	US-10-369-493-6861	Sequence 6861, Ap	1083	229.5	12.7	1117	4	US-10-435-751-166	Sequence 166, App
1013													

103	186	10.3	708	6	US-10-511-538-229	Sequence 229, App	179	151.5	8.4	344	7	US-11-186-284-20	Sequence 20, Appl
104	185.5	10.3	696	6	US-10-453-372-366	Sequence 366, App	180	151.5	8.4	344	7	US-11-077-386-16	Sequence 16, Appl
105	185.5	10.3	702	6	US-10-510-101-68	Sequence 68, Appl	181	151.5	8.4	344	7	US-11-097-224B-4	Sequence 4, Appl
106	185.5	10.3	702	7	US-11-033-039-282	Sequence 282, App	182	151.5	8.4	1363	7	US-11-043-693-32	Sequence 32, Appl
107	185.5	10.3	702	7	US-11-097-224B-2	Sequence 2, Appl1	183	150.5	8.3	555	6	US-10-821-234-1015	Sequence 1015, Ap
108	185	10.3	2630	7	US-11-186-731-2	Sequence 2, Appl1	184	150.5	8.3	777	7	US-11-043-693-3	Sequence 3, Appl1
109	184	10.2	670	6	US-10-453-372-710	Sequence 710, App	185	150.5	8.3	1298	7	US-11-076-427A-12	Sequence 12, Appl
110	184	10.2	757	6	US-10-453-372-320	Sequence 320, App	186	150.5	8.3	1362	7	US-11-043-693-33	Sequence 33, Appl
111	184	10.2	757	6	US-10-453-372-350	Sequence 350, App	187	150.5	8.3	1363	7	US-11-076-427A-10	Sequence 10, Appl
112	184	10.2	757	6	US-10-453-372-352	Sequence 352, App	188	150.5	8.3	1368	7	US-11-043-693-34	Sequence 34, Appl
113	184	10.2	763	6	US-10-453-372-328	Sequence 328, App	189	149.5	8.3	740	7	US-11-137-465-61	Sequence 61, Appl
114	184	10.2	773	6	US-10-453-372-348	Sequence 348, App	190	149.5	8.3	1250	7	US-11-137-465-62	Sequence 62, Appl
115	184	10.2	778	6	US-10-453-372-330	Sequence 330, App	191	145	8.0	259	7	US-11-000-463-216	Sequence 276, App
116	183	10.1	473	6	US-10-453-372-684	Sequence 684, App	192	145	8.0	972	6	US-10-821-234-1587	Sequence 1587, Ap
117	182	10.1	841	6	US-10-453-372-334	Sequence 334, App	193	142.5	7.9	739	6	US-10-493-909-69	Sequence 69, Appl
118	181.5	10.0	297	6	US-10-453-372-766	Sequence 766, App	194	142.5	7.9	739	7	US-11-107-028-6	Sequence 6, Appl1
119	181.5	10.0	469	6	US-10-453-372-344	Sequence 344, App	195	140.5	7.8	1089	7	US-11-148-770-32	Sequence 32, Appl
120	181	10.0	696	6	US-10-453-372-324	Sequence 324, App	196	140.5	7.8	1089	7	US-11-076-427A-14	Sequence 14, Appl
121	181	10.0	696	6	US-10-453-372-336	Sequence 336, App	197	140.5	7.8	1451	6	US-10-995-561-829	Sequence 829, App
122	181	10.0	696	6	US-10-453-372-346	Sequence 346, App	198	140	7.8	976	7	US-11-148-770-31	Sequence 31, Appl
123	181	10.0	696	6	US-10-453-372-354	Sequence 354, App	199	139.5	7.7	515	7	US-11-093-274-38	Sequence 38, Appl
124	181	10.0	696	6	US-10-453-372-356	Sequence 356, App	200	136.5	7.6	738	6	US-10-995-561-692	Sequence 692, App
125	181	10.0	696	6	US-10-453-372-360	Sequence 360, App	201	136.5	7.6	738	6	US-10-995-561-693	Sequence 693, App
126	181	10.0	696	6	US-10-453-372-362	Sequence 362, App	202	136	7.5	298	7	US-11-025-834A-14	Sequence 14, Appl
127	181	10.0	696	6	US-10-453-372-364	Sequence 364, App	203	134.5	7.4	419	6	US-10-821-234-1664	Sequence 1664, Ap
128	181	10.0	696	6	US-10-453-372-368	Sequence 368, App	204	134.5	7.4	647	7	US-11-080-991-32	Sequence 32, Appl
129	181	10.0	700	6	US-10-453-372-326	Sequence 326, App	206	131	7.3	1106	7	US-11-076-427A-16	Sequence 16, Appl
130	180.5	10.0	1256	6	US-10-493-909-90	Sequence 90, Appl	208	128	7.1	426	6	US-10-821-234-1585	Sequence 1585, Ap
131	179	9.9	696	6	US-10-453-372-358	Sequence 358, App	209	127	7.0	917	7	US-11-144-987-24	Sequence 24, Appl
132	179	9.9	917	6	US-10-493-909-76	Sequence 76, Appl	210	127	7.0	917	7	US-11-144-987-26	Sequence 26, Appl
133	178.5	9.9	1352	6	US-10-493-909-89	Sequence 89, Appl	211	126.5	7.0	365	7	US-11-102-978-9	Sequence 9, Appl1
134	177	9.8	300	7	US-11-025-834A-21	Sequence 21, Appl	212	126.5	7.0	365	7	US-11-080-991-78	Sequence 78, Appl
135	177	9.8	409	6	US-10-821-234-892	Sequence 892, App	213	125.5	6.9	416	6	US-10-453-372-1028	Sequence 1028, Ap
136	176	9.7	345	6	US-10-453-372-758	Sequence 758, App	214	125.5	6.9	448	6	US-10-453-372-1024	Sequence 1024, Ap
137	176	9.7	543	6	US-10-453-372-756	Sequence 756, App	215	125.5	6.9	451	6	US-10-453-372-1040	Sequence 1040, Ap
138	176	9.7	766	6	US-10-453-372-752	Sequence 752, App	216	125.5	6.9	454	6	US-10-453-372-1022	Sequence 1022, Ap
139	172	9.5	488	6	US-10-995-561-860	Sequence 860, App	217	125.5	6.9	456	6	US-10-453-372-1026	Sequence 1026, Ap
140	171.5	9.5	1338	7	US-11-109-156-23	Sequence 23, Appl	218	125.5	6.9	503	6	US-10-453-372-1020	Sequence 1020, Ap
141	171	9.5	917	6	US-10-493-909-87	Sequence 87, Appl	219	125.5	6.9	334	6	US-10-453-372-1038	Sequence 1038, Ap
142	169.5	9.4	1338	6	US-10-821-234-1622	Sequence 1622, Ap	220	124.5	6.9	321	7	US-11-159-919-2	Sequence 2, Appl1
143	167	9.2	764	7	US-11-104-110-8	Sequence 8, Appl1	221	123	6.8	399	7	US-11-159-919-4	Sequence 4, Appl1
144	167	9.2	764	7	US-11-104-111-28	Sequence 28, Appl	222	123	6.8	212	7	US-11-025-834A-16	Sequence 16, Appl
145	167	9.2	767	7	US-11-043-693-2	Sequence 2, Appl1	223	122	6.8	298	7	US-11-085-812-4	Sequence 4, Appl1
146	167	9.2	1306	6	US-10-995-561-905	Sequence 905, App	224	122	6.8	330	7	US-11-085-812-2	Sequence 2, Appl1
147	167	9.2	1356	6	US-10-995-561-904	Sequence 904, App	225	122	6.8	606	6	US-10-624-932-16	Sequence 16, Appl
148	167	9.2	1356	6	US-10-995-561-906	Sequence 906, App	226	122	6.8	606	6	US-10-624-932-18	Sequence 18, Appl
149	166.5	9.2	765	7	US-11-172-410-19	Sequence 19, Appl	227	122	6.8	915	7	US-11-144-987-22	Sequence 22, Appl
150	166	9.2	758	7	US-11-043-693-1	Sequence 1, Appl1	228	122	6.8	900	7	US-11-144-987-10	Sequence 10, Appl
151	165	9.1	822	7	US-11-183-567A-2	Sequence 2, Appl1	230	121	6.7	902	7	US-11-144-987-12	Sequence 12, Appl
152	164.5	9.1	438	7	US-11-186-541-2	Sequence 2, Appl1	231	121	6.7	902	7	US-11-144-987-14	Sequence 14, Appl
153	164.5	9.1	583	7	US-11-080-991-64	Sequence 64, Appl	232	121	6.7	915	7	US-11-144-987-16	Sequence 16, Appl
154	164	9.1	628	7	US-11-080-991-108	Sequence 108, App	233	120.5	6.7	917	7	US-11-144-987-18	Sequence 18, Appl
155	163	9.0	310	7	US-11-025-834A-13	Sequence 13, Appl	234	120.5	6.7	917	7	US-11-144-987-20	Sequence 20, Appl
156	163	9.0	924	7	US-11-107-028-26	Sequence 26, Appl	235	120.5	6.7	934	7	US-11-046-653-4	Sequence 4, Appl1
157	162.5	9.0	508	6	US-10-514-534-7	Sequence 7, Appl1	236	120	6.6	945	7	US-11-183-136-20	Sequence 20, Appl
158	162.5	9.0	508	7	US-11-093-274-41	Sequence 41, Appl	238	120	6.6	442	6	US-10-821-234-1594	Sequence 1594, Ap
160	161	8.9	310	7	US-11-025-834A-15	Sequence 15, Appl	239	119.5	6.6	910	7	US-11-144-987-2	Sequence 2, Appl1
161	161	8.9	362	6	US-10-821-234-1148	Sequence 1148, Ap	241	119	6.6	931	7	US-11-019-711-118	Sequence 118, App
162	161	8.9	842	7	US-11-124-368A-171	Sequence 171, App	242	118.5	6.6	931	7	US-11-019-711-119	Sequence 119, App
163	159.5	8.8	713	6	US-10-453-372-322	Sequence 322, App	243	118.5	6.6	931	7	US-11-019-711-120	Sequence 120, App
164	159	8.8	924	6	US-10-857-780-20	Sequence 20, Appl	244	118.5	6.6	931	7	US-11-183-136-24	Sequence 24, Appl
165	159	8.8	924	6	US-10-493-909-67	Sequence 67, Appl	245	118.5	6.6	266	6	US-10-995-561-544	Sequence 544, App
166	158.5	8.8	912	6	US-10-493-909-75	Sequence 75, Appl	246	117.5	6.5	505	6	US-10-493-909-81	Sequence 81, Appl
168	157	8.7	299	7	US-11-000-463-275	Sequence 275, App	247	117.5	6.5	900	7	US-11-144-987-4	Sequence 4, Appl1
169	157	8.7	299	7	US-11-000-463-747	Sequence 747, App	248	117.5	6.5	902	7	US-11-144-987-6	Sequence 6, Appl1
170	157	8.7	299	7	US-11-000-463-748	Sequence 748, App	249	117.5	6.5	902	7	US-11-144-987-8	Sequence 8, Appl1
171	157	8.7	299	7	US-11-173-037-7	Sequence 7, Appl1	250	117.5	6.5	267	6	US-10-995-561-543	Sequence 543, App
172	157	8.7	734	7	US-11-093-274-40	Sequence 40, Appl	251	117	6.5	479	7	US-11-147-047-44	Sequence 44, Appl
174	155	8.6	977	7	US-11-093-274-39	Sequence 39, Appl	253	115	6.4	628	6	US-10-453-372-548	Sequence 548, App
175	154.5	8.6	1897	6	US-10-821-234-1635	Sequence 1635, Ap	254	115	6.4	628	6	US-10-453-372-550	Sequence 550, App
176	154.5	8.6	1907	7	US-11-000-463-250	Sequence 250, App	255	115	6.4	628	7	US-11-147-047-45	Sequence 45, Appl
177	151.5	8.4	324	7	US-11-077-386-15	Sequence 15, Appl	256	115	6.4	189	6	US-10-453-372-338	Sequence 338, App
178	151.5	8.4	344	7	US-11-080-991-4	Sequence 4, Appl1	257	114.5	6.3				

258	114.5	6.3	189	6	US-10-453-372-340	Sequence 340, App	334	99	5.5	595	7	US-11-102-476-33	Sequence 33, Appl
259	114.5	6.3	189	6	US-10-453-372-342	Sequence 342, App	335	99	5.5	1225	7	US-11-102-476-2	Sequence 2, Appli
260	114	6.3	799	6	US-10-493-909-8	Sequence 8, Appli	336	98.5	5.5	220	7	US-11-174-150-32	Sequence 32, Appl
261	114	6.3	822	6	US-10-493-909-48	Sequence 48, Appl	337	98	5.4	535	6	US-10-493-909-84	Sequence 84, Appl
262	113.5	6.3	547	6	US-10-995-561-785	Sequence 785, App	338	98	5.4	544	6	US-10-493-909-73	Sequence 73, Appl
263	113.5	6.3	547	6	US-10-995-561-787	Sequence 787, App	339	97.5	5.4	374	7	US-11-000-463-453	Sequence 453, App
264	113.5	6.3	547	6	US-10-493-909-65	Sequence 65, Appl	340	97.5	5.4	592	7	US-11-135-855-24	Sequence 24, Appl
265	113.5	6.3	547	7	US-11-107-028-24	Sequence 24, Appl	341	97.5	5.4	597	6	US-10-884-730-381	Sequence 381, App
266	113	6.3	458	7	US-11-016-503-12	Sequence 12, Appl	342	97.5	5.4	824	7	US-11-116-939-11	Sequence 11, Appl
267	113	6.3	458	7	US-11-089-803-2	Sequence 2, Appli	343	97	5.4	359	7	US-11-087-177-29	Sequence 29, Appl
268	113	6.3	467	7	US-11-000-463-452	Sequence 452, App	344	97	5.4	406	7	US-11-000-463-377	Sequence 377, App
269	113	6.3	467	7	US-11-000-463-924	Sequence 924, App	345	97	5.4	406	7	US-11-000-463-849	Sequence 849, App
270	113	6.3	467	7	US-11-000-463-925	Sequence 925, App	346	96.5	5.3	359	6	US-10-055-877-265	Sequence 265, App
271	113	6.3	551	7	US-11-000-463-346	Sequence 346, App	348	96.5	5.3	359	7	US-11-080-091-1	Sequence 1, Appli
272	111.5	6.2	240	7	US-11-089-803-23	Sequence 23, Appl	349	96.5	5.3	359	7	US-11-116-939-15	Sequence 15, Appl
273	111.5	6.2	430	7	US-11-016-503-17	Sequence 17, Appl	350	96.5	5.3	359	7	US-11-087-177-23	Sequence 23, Appl
274	111.5	6.2	430	7	US-11-016-503-16	Sequence 16, Appl	351	96.5	5.3	447	6	US-10-493-909-82	Sequence 82, Appl
275	111.5	6.2	458	7	US-11-089-803-6	Sequence 6, Appli	352	96	5.3	334	7	US-11-113-424-80	Sequence 80, Appl
276	111.5	6.2	458	7	US-11-149-738-2	Sequence 2, Appli	353	96	5.3	527	7	US-11-113-424-81	Sequence 81, Appl
277	111.5	6.2	458	7	US-11-155-269-2	Sequence 2, Appli	354	96	5.3	548	6	US-10-493-909-77	Sequence 77, Appl
278	111.5	6.2	458	7	US-11-193-746-2	Sequence 2, Appli	355	96	5.3	575	6	US-10-453-372-78	Sequence 78, Appl
279	111	6.1	398	6	US-10-821-234-1583	Sequence 1583, Ap	356	95	5.3	282	7	US-11-186-284-85	Sequence 85, Appl
280	111	6.1	471	7	US-11-086-289-6	Sequence 6, Appli	358	94	5.2	222	6	US-10-453-372-844	Sequence 844, App
281	109.5	6.1	444	7	US-11-043-788-311	Sequence 311, App	359	94	5.2	283	6	US-10-453-372-850	Sequence 850, App
282	110.5	6.1	931	7	US-11-019-711-117	Sequence 117, App	360	94	5.2	230	6	US-10-453-372-836	Sequence 836, App
283	110.5	6.1	931	7	US-11-183-136-22	Sequence 22, Appl	361	94	5.2	230	6	US-10-453-372-842	Sequence 842, App
284	110	6.1	948	6	US-10-016-686-3	Sequence 3, Appli	362	94	5.2	290	6	US-10-453-372-848	Sequence 848, App
285	110	6.1	945	7	US-11-019-711-38	Sequence 38, Appl	363	94	5.2	220	7	US-11-113-424-77	Sequence 77, Appl
286	110	6.1	1579	7	US-11-052-554-9	Sequence 9, Appli	363	94	5.2	220	6	US-10-453-372-840	Sequence 840, App
287	109.5	6.1	444	7	US-11-043-788-311	Sequence 311, App	364	94	5.2	295	6	US-11-116-939-10	Sequence 10, Appl
288	109.5	6.1	532	6	US-10-857-780-18	Sequence 18, Appl	365	93.5	5.2	293	7	US-11-198-819-14	Sequence 14, Appl
289	109.5	6.1	532	6	US-10-995-561-897	Sequence 897, App	366	92.5	5.1	431	7	US-11-198-819-20	Sequence 20, Appl
290	109.5	6.1	532	6	US-10-493-909-2	Sequence 2, Appli	367	92.5	5.1	431	7	US-11-198-819-14	Sequence 14, Appl
291	109.5	6.1	532	6	US-10-493-909-63	Sequence 63, Appl	368	92.5	5.1	592	6	US-10-016-686-4	Sequence 4, Appli
292	109.5	6.1	532	7	US-11-104-812-2	Sequence 2, Appli	369	92.5	5.1	615	7	US-11-198-819-16	Sequence 16, Appl
293	109.5	6.1	532	7	US-11-105-279-2	Sequence 2, Appli	370	92.5	5.1	615	7	US-11-198-819-18	Sequence 18, Appl
294	109.5	6.1	532	7	US-11-107-028-22	Sequence 22, Appl	371	92	5.1	285	5	US-09-978-360A-489	Sequence 489, App
295	109.5	6.1	532	7	US-11-043-788-307	Sequence 307, App	372	92	5.1	338	7	US-11-124-367A-471	Sequence 471, App
296	109.5	6.1	532	7	US-11-043-788-308	Sequence 308, App	373	92	5.1	545	6	US-10-493-909-86	Sequence 86, Appl
297	109.5	6.1	533	7	US-11-147-047-33	Sequence 33, Appl	374	91.5	5.1	762	6	US-11-116-939-13	Sequence 13, Appl
298	109.5	6.1	771	7	US-11-147-047-34	Sequence 34, Appl	375	91	5.0	287	6	US-10-453-372-70	Sequence 70, Appl
299	109	6.0	429	7	US-11-093-274-37	Sequence 37, Appl	376	91	5.0	365	7	US-11-087-177-27	Sequence 27, Appl
300	108	6.0	77	7	US-11-113-424-189	Sequence 189, App	377	91	5.0	550	6	US-10-453-372-76	Sequence 76, Appl
301	107.5	6.0	468	7	US-11-086-289-14	Sequence 14, Appl	378	91	5.0	578	6	US-10-453-372-66	Sequence 66, Appl
302	106.5	5.9	766	7	US-11-147-047-27	Sequence 27, Appl	379	91	5.0	578	6	US-10-453-372-80	Sequence 80, Appl
303	106	5.9	347	6	US-10-453-372-490	Sequence 490, App	380	90.5	5.0	258	7	US-11-054-515-2083	Sequence 2083, Ap
304	106	5.9	347	6	US-10-453-372-500	Sequence 500, App	381	90.5	5.0	275	7	US-11-113-424-79	Sequence 79, Appl
305	105	5.8	269	6	US-10-821-234-1308	Sequence 1308, App	382	90.5	5.0	282	7	US-11-102-240-60	Sequence 60, Appl
306	105	5.8	334	6	US-10-689-742-134	Sequence 134, App	383	90.5	5.0	312	7	US-11-000-463-334	Sequence 334, App
307	104.5	5.8	336	7	US-11-113-424-83	Sequence 83, Appl	384	90.5	5.0	500	6	US-10-453-372-492	Sequence 492, App
308	104	5.8	529	7	US-11-113-424-82	Sequence 82, Appl	385	90.5	5.0	500	6	US-10-453-372-504	Sequence 504, App
309	103.5	5.7	455	7	US-11-016-503-14	Sequence 14, Appl	386	90.5	5.0	500	6	US-11-102-240-84	Sequence 84, Appl
310	103.5	5.7	455	7	US-11-089-803-4	Sequence 4, Appli	388	90.5	5.0	524	6	US-10-995-561-789	Sequence 789, App
311	103.5	5.7	945	7	US-11-019-711-121	Sequence 121, App	390	90	5.0	258	7	US-11-054-515-1234	Sequence 1234, Ap
312	103	5.7	247	7	US-11-113-424-76	Sequence 76, Appl	391	90	5.0	614	7	US-11-165-576-2	Sequence 2, Appli
313	102	5.6	63	7	US-11-019-711-128	Sequence 128, App	392	90	5.0	614	7	US-11-165-576-4	Sequence 1698, Ap
314	102	5.6	273	7	US-11-113-424-74	Sequence 74, Appl	394	89	4.9	240	7	US-11-054-515-1898	Sequence 3, Appli
315	102	5.6	273	7	US-11-113-424-75	Sequence 75, Appl	395	89	4.9	313	6	US-10-723-207-3	Sequence 1102, Ap
316	102	5.6	537	6	US-10-493-909-74	Sequence 74, Appl	396	89	4.9	1452	6	US-10-821-234-1102	Sequence 1402, Ap
317	101.5	5.6	246	6	US-10-016-686-10	Sequence 10, Appl	397	88.5	4.9	214	6	US-10-453-372-498	Sequence 498, App
318	101.5	5.6	329	7	US-11-029-188-4	Sequence 4, Appli	398	88.5	4.9	230	7	US-11-098-686-10984	Sequence 10984, A
319	101.5	5.6	412	7	US-11-116-939-12	Sequence 12, Appl	399	88.5	4.9	251	7	US-11-054-515-279	Sequence 279, App
320	101.5	5.6	945	7	US-11-183-136-18	Sequence 18, Appl	400	88.5	4.9	251	7	US-11-054-515-316	Sequence 316, App
321	100.5	5.6	346	7	US-11-174-150-33	Sequence 33, Appl	401	88.5	4.9	463	7	US-11-128-900-4	Sequence 4, Appli
322	100.5	5.6	391	6	US-10-996-628-2	Sequence 2, Appli	402	88.5	4.9	463	7	US-11-128-900-68	Sequence 68, Appl
323	100.5	5.6	716	7	US-11-147-047-52	Sequence 52, Appl	404	88.5	4.9	466	7	US-11-102-240-104	Sequence 104, App
324	100.5	5.6	716	7	US-11-142-867-2	Sequence 2, Appli	405	88.5	4.9	548	7	US-11-137-465-47	Sequence 47, Appl
325	100.5	5.6	398	6	US-10-996-628-4	Sequence 4, Appli	406	88	4.9	178	6	US-10-453-372-838	Sequence 838, App
326	100	5.5	537	6	US-10-493-909-70	Sequence 70, Appl	407	88	4.9	178	6	US-10-453-372-846	Sequence 846, App
327	100	5.5	537	6	US-10-493-909-78	Sequence 78, Appl	408	88	4.9	249	7	US-11-113-424-30	Sequence 30, Appl
328	100	5.5	548	6	US-10-493-909-78	Sequence 78, Appl	408	88	4.9	249	7	US-11-113-424-78	Sequence 78, Appl
329	99.5	5.5	288	6	US-10-821-234-1062	Sequence 1062, Ap	409	88	4.9	290	7	US-11-128-900-100	Sequence 100, App
330	99.5	5.5	543	6	US-10-495-664-3	Sequence 3, Appli	410	88	4.9	364	7	US-11-198-819-22	Sequence 22, Appl
331	99	5.5	359	7	US-11-087-177-25	Sequence 25, Appl	411	88	4.9	651	7	US-11-198-819-22	Sequence 52, Appl
332	99	5.5	537	6	US-10-493-909-71	Sequence 71, Appl	412	87.5	4.8	102	7	US-11-043-693-52	Sequence 52, Appl
333	99	5.5	537	6	US-10-493-909-71	Sequence 71, Appl	412	87.5	4.8	102	7	US-11-043-693-52	Sequence 52, Appl

413	87.5	4.8	252	7	US-11-054-515-1401	Sequence 1401, Ap	487	82.5	4.6	463	7	US-11-128-900-1	Sequence 1, Appl
414	87.5	4.8	382	7	US-11-179-411-22	Sequence 22, Appl	488	82.5	4.6	463	7	US-11-128-900-63	Sequence 63, Appl
415	87.5	4.8	382	7	US-11-175-766-22	Sequence 22, Appl	489	82.5	4.6	470	7	US-11-144-228-45	Sequence 45, Appl
416	87	4.8	252	7	US-11-054-515-988	Sequence 988, Ap	490	82.5	4.6	470	7	US-11-144-228-45	Sequence 45, Appl
417	87	4.8	527	6	US-10-493-909-66	Sequence 66, Appl	491	82.5	4.6	470	7	US-11-182-343-45	Sequence 45, Appl
418	87	4.8	577	6	US-10-493-909-72	Sequence 72, Appl	492	82.5	4.6	1263	6	US-10-485-517-137	Sequence 127, App
419	86.5	4.8	232	7	US-11-000-463-755	Sequence 755, App	493	82	4.5	245	6	US-10-902-546-13	Sequence 13, Appl
420	86.5	4.8	251	7	US-11-054-515-64	Sequence 64, Appl	494	82	4.5	251	6	US-10-902-546-13	Sequence 13, Appl
421	86.5	4.8	414	7	US-11-043-788-310	Sequence 310, App	495	82	4.5	251	7	US-11-054-515-136	Sequence 196, App
422	86.5	4.8	443	6	US-10-793-626-1860	Sequence 1860, Ap	496	82	4.5	288	7	US-11-029-188-2	Sequence 2, Appl
423	86.5	4.8	530	6	US-10-493-909-85	Sequence 85, Appl	497	81.5	4.5	244	7	US-11-054-515-1924	Sequence 10, Appl
424	86	4.8	243	6	US-10-016-686-1	Sequence 1, Appl	498	81.5	4.5	246	7	US-11-054-515-1268	Sequence 1268, Ap
425	86	4.8	250	7	US-11-054-515-78	Sequence 78, Appl	499	81.5	4.5	251	7	US-11-054-515-71	Sequence 71, Appl
426	86	4.6	253	7	US-11-054-515-1829	Sequence 1829, Ap	500	81.5	4.5	251	7	US-11-054-515-83	Sequence 83, Appl
427	86	4.8	256	7	US-11-054-515-1791	Sequence 1791, Ap	501	81.5	4.5	251	7	US-11-054-515-229	Sequence 229, App
428	86	4.8	394	7	US-11-098-686-10449	Sequence 10449, A	502	81.5	4.5	251	7	US-11-054-515-288	Sequence 288, App
429	86	4.8	2455	7	US-11-186-999-4	Sequence 4, Appl	503	81.5	4.5	251	7	US-11-054-515-300	Sequence 300, App
430	85.5	4.7	251	7	US-11-054-515-114	Sequence 114, App	504	81	4.5	108	7	US-11-049-536-260	Sequence 260, App
431	85.5	4.7	500	6	US-10-453-372-502	Sequence 502, App	505	81	4.5	241	7	US-11-054-515-2055	Sequence 2055, Ap
432	85.5	4.7	602	6	US-10-493-909-51	Sequence 51, Appl	506	81	4.5	245	7	US-11-019-027-73	Sequence 73, Appl
433	85.5	4.7	1254	6	US-10-528-031-47	Sequence 47, Appl	507	81	4.5	247	7	US-11-054-515-2092	Sequence 2092, Ap
434	85	4.7	251	7	US-11-054-515-67	Sequence 67, Appl	508	81	4.5	247	7	US-11-054-515-2103	Sequence 2103, Ap
435	85	4.7	464	7	US-11-128-900-2	Sequence 2, Appl	509	81	4.5	250	7	US-11-054-515-59	Sequence 59, Appl
436	85	4.7	464	7	US-11-128-900-66	Sequence 66, Appl	510	81	4.5	251	7	US-11-054-515-6	Sequence 6, Appl
437	85	4.7	1026	7	US-11-154-227-95	Sequence 95, Appl	511	81	4.5	348	6	US-10-793-626-2866	Sequence 2866, Ap
438	85	4.7	1060	7	US-11-090-739-120	Sequence 120, App	512	81	4.5	410	6	US-10-793-626-3258	Sequence 3258, Ap
439	85	4.7	1203	6	US-11-154-227-103	Sequence 103, App	513	81	4.5	472	7	US-11-086-289-10	Sequence 10, Appl
440	85	4.7	1206	6	US-10-995-561-709	Sequence 709, App	514	81	4.5	472	6	US-10-793-626-3250	Sequence 3250, Ap
441	85	4.7	1307	6	US-10-995-561-711	Sequence 711, App	515	81	4.5	2458	7	US-11-186-999-11	Sequence 11, Appl
442	85	4.7	2256	7	US-11-144-368-4	Sequence 4, Appl	516	80.5	4.5	246	7	US-11-054-515-1913	Sequence 1913, Ap
443	85	4.7	2458	7	US-11-186-999-6	Sequence 6, Appl	517	80.5	4.5	249	7	US-11-054-515-389	Sequence 389, App
444	85	4.7	2458	7	US-11-186-999-13	Sequence 13, Appl	518	80.5	4.5	250	7	US-11-054-515-110	Sequence 110, App
445	85	4.7	2483	7	US-11-186-999-2	Sequence 2, Appl	519	80.5	4.5	251	7	US-11-054-515-117	Sequence 117, App
446	85	4.7	3377	7	US-11-124-367A-271	Sequence 271, App	520	80.5	4.5	251	7	US-11-054-515-118	Sequence 118, App
447	85	4.7	3841	7	US-11-124-367A-272	Sequence 272, App	521	80.5	4.5	251	7	US-11-054-515-138	Sequence 138, App
448	84.5	4.7	245	7	US-11-054-515-1615	Sequence 1615, Ap	522	80.5	4.5	258	7	US-11-054-515-1173	Sequence 1173, Ap
449	84.5	4.7	248	7	US-11-054-515-1615	Sequence 1615, Ap	523	80.5	4.5	251	7	US-11-128-900-70	Sequence 70, Appl
450	84.5	4.7	259	6	US-10-995-561-1665	Sequence 883, App	524	80.5	4.5	535	7	US-11-106-672A-44	Sequence 44, Appl
451	84.5	4.7	305	7	US-11-080-091-13	Sequence 13, Appl	525	80	4.4	239	6	US-10-995-561-734	Sequence 734, App
452	84.5	4.7	305	7	US-11-087-177-11	Sequence 11, Appl	526	80	4.4	239	6	US-10-995-561-737	Sequence 737, App
453	84.5	4.7	305	7	US-11-087-177-13	Sequence 13, Appl	527	80	4.4	244	7	US-11-054-515-1513	Sequence 1513, Ap
454	84.5	4.7	328	6	US-10-995-561-884	Sequence 884, App	528	80	4.4	246	7	US-11-054-515-1917	Sequence 1917, Ap
455	84.5	4.7	364	7	US-11-087-177-31	Sequence 31, Appl	529	80	4.4	251	7	US-11-054-515-262	Sequence 262, App
456	84	4.7	252	7	US-11-054-515-1541	Sequence 1541, Ap	530	80	4.4	251	7	US-11-054-515-1510	Sequence 1510, Ap
458	84	4.7	745	7	US-11-135-855-37	Sequence 37, Appl	531	80	4.4	254	7	US-11-054-515-1447	Sequence 1447, Ap
459	83.5	4.6	234	7	US-11-139-499-2	Sequence 2, Appl	532	80	4.4	287	6	US-10-995-561-730	Sequence 730, App
460	83.5	4.6	243	7	US-11-054-515-1909	Sequence 1909, Ap	533	80	4.4	452	7	US-11-016-503-6	Sequence 6, Appl
461	83.5	4.6	244	7	US-11-054-515-1606	Sequence 1606, Ap	534	80	4.4	514	6	US-10-821-234-998	Sequence 998, App
462	83.5	4.6	249	7	US-11-054-515-665	Sequence 665, App	535	80	4.4	557	7	US-11-016-503-4	Sequence 4, Appl
463	83.5	4.6	251	7	US-11-054-515-210	Sequence 210, App	536	80	4.4	567	7	US-11-016-503-2	Sequence 2, Appl
464	83.5	4.6	294	6	US-10-955-877-128	Sequence 128, App	537	80	4.4	995	7	US-11-113-424-62	Sequence 62, Appl
465	83.5	4.6	307	6	US-10-955-877-263	Sequence 263, App	538	79.5	4.4	215	6	US-10-374-954-7	Sequence 7, Appl
466	83.5	4.6	364	7	US-11-087-177-33	Sequence 33, Appl	539	79.5	4.4	243	7	US-11-054-515-2051	Sequence 521, Ap
467	83	4.6	238	7	US-11-158-505-9	Sequence 9, Appl	540	79.5	4.4	250	7	US-11-054-515-52	Sequence 52, Appl
468	83	4.6	238	7	US-11-158-505-11	Sequence 11, Appl	541	79.5	4.4	250	7	US-11-054-515-899	Sequence 899, App
469	83	4.6	238	7	US-11-158-505-17	Sequence 17, Appl	542	79.5	4.4	251	7	US-11-054-515-22	Sequence 22, Appl
470	83	4.6	238	7	US-11-158-505-19	Sequence 19, Appl	543	79.5	4.4	251	7	US-11-054-515-24	Sequence 24, Appl
471	83	4.6	238	7	US-11-158-505-74	Sequence 74, Appl	544	79.5	4.4	251	7	US-11-054-515-26	Sequence 26, Appl
472	83	4.6	249	7	US-11-054-515-2120	Sequence 2120, Ap	545	79.5	4.4	251	7	US-11-054-515-28	Sequence 28, Appl
473	83	4.6	290	7	US-11-032-773-957	Sequence 957, App	546	79.5	4.4	251	7	US-11-054-515-30	Sequence 30, Appl
474	83	4.6	319	7	US-11-032-773-955	Sequence 955, App	547	79.5	4.4	251	7	US-11-054-515-39	Sequence 39, Appl
475	83	4.6	473	7	US-11-144-248-50	Sequence 50, Appl	548	79.5	4.4	251	7	US-11-054-515-154	Sequence 154, App
476	83	4.6	473	7	US-11-144-222-50	Sequence 50, Appl	549	79.5	4.4	252	7	US-11-054-515-1416	Sequence 1416, Ap
477	83	4.6	473	7	US-11-182-343-50	Sequence 50, Appl	550	79.5	4.4	326	7	US-11-103-621-34	Sequence 34, Appl
478	82.5	4.6	107	7	US-11-149-943-56	Sequence 56, Appl	552	79.5	4.4	463	7	US-11-102-240-86	Sequence 86, Appl
479	82.5	4.6	239	7	US-11-139-499-6	Sequence 6, Appl	553	79.5	4.4	567	6	US-11-000-463-400	Sequence 400, App
480	82.5	4.6	243	7	US-11-054-515-2056	Sequence 2056, Ap	554	79.5	4.4	766	6	US-10-522-789-2	Sequence 2, Appl
481	82.5	4.6	247	7	US-11-054-515-1527	Sequence 1527, Ap	555	79	4.4	144	7	US-11-055-163-16	Sequence 16, Appl
482	82.5	4.6	248	7	US-11-054-515-1360	Sequence 1360, Ap	556	79	4.4	238	7	US-11-158-505-1	Sequence 1, Appl
483	82.5	4.6	250	7	US-11-054-515-1280	Sequence 1280, Ap	557	79	4.4	238	7	US-11-158-505-3	Sequence 3, Appl
484	82.5	4.6	254	7	US-11-054-515-1302	Sequence 1302, Ap	558	79	4.4	238	7	US-11-158-505-25	Sequence 25, Appl
485	82.5	4.6	254	7	US-11-054-515-1843	Sequence 1843, Ap	559	79	4.4	238	7	US-11-158-505-27	Sequence 27, Appl
486	82.5	4.6	463	7	US-11-000-463-872	Sequence 872, App	560	79	4.4	249	7	US-11-054-515-1894	Sequence 1894, Ap

854	77.5	4.3	1532	7	US-11-124-367A-405	Sequence 405, App	927	76	4.2	251	7	US-11-054-515-88	Sequence 88, Appl
855	77.5	4.3	1532	7	US-11-124-367A-407	Sequence 407, App	928	76	4.2	251	7	US-11-054-515-240	Sequence 240, App
856	77.5	4.3	1535	7	US-11-124-367A-408	Sequence 408, App	929	76	4.2	251	7	US-11-054-515-2128	Sequence 2128, Ap
857	77	4.3	109	7	US-11-049-536-400	Sequence 400, App	930	76	4.2	252	7	US-11-054-515-1634	Sequence 1634, Ap
858	77	4.3	111	7	US-11-004-590-148	Sequence 148, App	931	76	4.2	255	7	US-11-054-515-1054	Sequence 1054, Ap
859	77	4.3	219	6	US-10-997-065-46	Sequence 46, Appl	932	76	4.2	263	6	US-10-512-184-29	Sequence 29, Appl
860	77	4.3	220	6	US-10-997-065-54	Sequence 54, Appl	933	76	4.2	359	7	US-11-098-686-10089	Sequence 10089, A
861	77	4.3	239	7	US-11-054-515-2022	Sequence 2022, App	934	76	4.2	450	7	US-11-025-712-12	Sequence 12, Appl
862	77	4.3	249	7	US-11-054-515-1024	Sequence 1024, Ap	935	76	4.2	618	6	US-10-512-184-48	Sequence 48, Appl
863	77	4.3	249	7	US-11-054-515-1024	Sequence 1024, Ap	936	75.5	4.2	213	7	US-11-172-320-8	Sequence 8, Appll
864	77	4.3	251	7	US-11-054-515-192	Sequence 192, App	937	75.5	4.2	213	7	US-11-173-969-8	Sequence 8, Appll
865	77	4.3	251	7	US-11-054-515-1555	Sequence 1555, Ap	938	75.5	4.2	235	7	US-11-166-994-2	Sequence 2, Appll
866	77	4.3	251	7	US-11-054-515-2125	Sequence 2125, Ap	939	75.5	4.2	245	7	US-11-054-515-3241	Sequence 3241, Ap
867	77	4.3	252	7	US-11-054-515-1223	Sequence 1223, Ap	940	75.5	4.2	248	7	US-11-054-515-914	Sequence 914, App
868	77	4.3	406	6	US-10-493-909-68	Sequence 68, Appl	941	75.5	4.2	248	7	US-11-054-515-1323	Sequence 1323, Ap
869	77	4.3	406	7	US-11-107-028-7	Sequence 7, Appll	942	75.5	4.2	249	7	US-11-054-515-542	Sequence 542, App
870	77	4.3	444	7	US-11-172-320-6	Sequence 6, Appll	943	75.5	4.2	250	7	US-11-054-515-53	Sequence 53, Appl
871	77	4.3	444	7	US-11-173-969-6	Sequence 6, Appll	944	75.5	4.2	251	7	US-11-054-515-23	Sequence 23, Appl
872	77	4.3	470	7	US-11-086-289-18	Sequence 18, Appl	945	75.5	4.2	251	7	US-11-054-515-25	Sequence 25, Appl
873	77	4.3	817	6	US-10-453-372-520	Sequence 520, App	946	75.5	4.2	251	7	US-11-054-515-27	Sequence 27, Appl
874	76.5	4.2	110	7	US-11-064-174-67	Sequence 67, Appl	947	75.5	4.2	251	7	US-11-054-515-29	Sequence 29, Appl
875	76.5	4.2	236	7	US-11-144-248-51	Sequence 51, Appl	948	75.5	4.2	251	7	US-11-054-515-31	Sequence 31, Appl
876	76.5	4.2	236	7	US-11-144-222-51	Sequence 51, Appl	949	75.5	4.2	251	7	US-11-054-515-120	Sequence 120, App
877	76.5	4.2	236	7	US-11-182-343-51	Sequence 51, Appl	950	75.5	4.2	251	7	US-11-054-515-128	Sequence 128, App
878	76.5	4.2	239	7	US-11-086-289-12	Sequence 12, Appl	951	75.5	4.2	251	7	US-11-054-515-141	Sequence 141, App
879	76.5	4.2	243	7	US-11-054-515-995	Sequence 995, App	952	75.5	4.2	251	7	US-11-054-515-202	Sequence 202, App
880	76.5	4.2	245	7	US-11-054-515-1926	Sequence 1926, Ap	953	75.5	4.2	251	7	US-11-054-515-209	Sequence 209, App
881	76.5	4.2	248	7	US-11-054-515-1237	Sequence 1237, Ap	954	75.5	4.2	251	7	US-11-054-515-223	Sequence 223, App
882	76.5	4.2	248	7	US-11-054-515-1386	Sequence 1386, Ap	955	75.5	4.2	252	7	US-11-054-515-320	Sequence 320, App
883	76.5	4.2	249	7	US-11-054-515-407	Sequence 407, App	956	75.5	4.2	252	7	US-11-054-515-1329	Sequence 1329, Ap
884	76.5	4.2	249	7	US-11-054-515-492	Sequence 492, App	957	75.5	4.2	252	7	US-11-054-515-1656	Sequence 1656, Ap
885	76.5	4.2	251	7	US-11-054-515-125	Sequence 125, App	958	75.5	4.2	253	7	US-11-054-515-934	Sequence 934, App
886	76.5	4.2	251	7	US-11-054-515-147	Sequence 147, App	959	75.5	4.2	258	7	US-11-054-515-1245	Sequence 1245, Ap
887	76.5	4.2	251	7	US-11-054-515-163	Sequence 163, App	960	75.5	4.2	341	6	US-10-514-534-6	Sequence 6, Appll
888	76.5	4.2	251	7	US-11-054-515-167	Sequence 167, App	961	75.5	4.2	442	7	US-11-102-621-126	Sequence 126, App
889	76.5	4.2	251	7	US-11-054-515-176	Sequence 176, App	962	75.5	4.2	476	7	US-11-139-499-12	Sequence 12, Appl
890	76.5	4.2	251	7	US-11-054-515-179	Sequence 179, App	963	75.5	4.2	544	7	US-11-052-554A-358	Sequence 358, App
891	76.5	4.2	251	7	US-11-054-515-208	Sequence 193, App	964	75.5	4.2	562	7	US-11-065-943-24	Sequence 24, Appll
892	76.5	4.2	251	7	US-11-054-515-208	Sequence 208, App	965	75.5	4.2	886	7	US-11-192-219-3	Sequence 3, Appll
893	76.5	4.2	251	7	US-11-054-515-258	Sequence 258, App	966	75.5	4.2	898	7	US-11-166-730-3	Sequence 3, Appll
894	76.5	4.2	251	7	US-11-054-515-268	Sequence 268, App	967	75.5	4.2	923	7	US-11-192-219-4	Sequence 4, Appll
895	76.5	4.2	251	7	US-11-054-515-278	Sequence 278, App	968	75.5	4.2	928	6	US-10-880-144-4	Sequence 4, Appll
896	76.5	4.2	251	7	US-11-054-515-287	Sequence 285, App	969	75.5	4.2	1165	7	US-11-192-219-2	Sequence 2, Appll
897	76.5	4.2	251	7	US-11-054-515-287	Sequence 287, App	970	75.5	4.2	2050	6	US-10-453-372-192	Sequence 192, App
898	76.5	4.2	251	7	US-11-054-515-298	Sequence 298, App	971	75.5	4.2	3568	6	US-10-453-372-194	Sequence 194, App
899	76.5	4.2	251	7	US-11-054-515-302	Sequence 302, App	972	75.5	4.2	3570	6	US-10-453-372-178	Sequence 178, App
900	76.5	4.2	251	7	US-11-054-515-307	Sequence 307, App	973	75.5	4.2	3570	6	US-10-453-372-196	Sequence 196, App
901	76.5	4.2	251	7	US-11-054-515-310	Sequence 310, App	974	75.5	4.2	3570	6	US-10-453-372-198	Sequence 198, App
902	76.5	4.2	251	7	US-11-054-515-314	Sequence 314, App	975	75.5	4.2	3570	6	US-10-453-372-200	Sequence 200, App
903	76.5	4.2	251	7	US-11-054-515-1309	Sequence 1309, Ap	976	75.5	4.2	3570	6	US-10-453-372-202	Sequence 202, App
904	76.5	4.2	252	7	US-11-054-515-1366	Sequence 1366, Ap	977	75.5	4.2	3570	6	US-10-453-372-204	Sequence 204, App
905	76.5	4.2	253	7	US-11-054-515-1545	Sequence 1545, Ap	978	75.5	4.2	3570	6	US-10-453-372-206	Sequence 206, App
906	76.5	4.2	310	6	US-11-000-463-357	Sequence 357, App	979	75	4.2	106	7	US-11-107-028-34	Sequence 34, Appl
907	76.5	4.2	331	6	US-10-453-372-508	Sequence 508, App	980	75	4.2	214	7	US-11-102-621-129	Sequence 129, App
908	76.5	4.2	899	6	US-10-493-909-83	Sequence 83, Appl	981	75	4.2	236	7	US-11-054-515-2010	Sequence 1988, Ap
909	76.5	4.2	899	6	US-10-453-372-506	Sequence 506, App	982	75	4.2	241	7	US-11-054-515-1888	Sequence 1888, Ap
910	76.5	4.2	899	6	US-10-453-372-524	Sequence 524, App	983	75	4.2	247	7	US-11-054-515-1328	Sequence 1328, Ap
911	76.5	4.2	899	6	US-10-453-372-526	Sequence 526, App	984	75	4.2	247	7	US-11-054-515-1685	Sequence 1685, App
912	76.5	4.2	899	6	US-10-453-372-528	Sequence 528, App	985	75	4.2	251	7	US-11-054-515-925	Sequence 925, App
913	76.5	4.2	899	6	US-10-453-372-530	Sequence 530, App	986	75	4.2	252	7	US-11-054-515-1169	Sequence 1169, Ap
914	76.5	4.2	899	6	US-10-453-372-532	Sequence 532, App	987	75	4.2	253	7	US-11-054-515-1619	Sequence 1619, Ap
915	76.5	4.2	899	6	US-10-453-372-534	Sequence 534, App	988	75	4.2	253	7	US-11-054-515-1777	Sequence 1777, Ap
916	76.5	4.2	899	6	US-10-453-372-536	Sequence 536, App	989	75	4.2	258	7	US-11-054-515-1799	Sequence 1799, Ap
917	76.5	4.2	899	6	US-10-453-372-538	Sequence 538, App	990	75	4.2	279	6	US-10-793-626-870	Sequence 870, App
918	76.5	4.2	899	6	US-10-453-372-540	Sequence 540, App	991	75	4.2	343	7	US-11-016-564-15	Sequence 15, Appl
919	76.5	4.2	899	6	US-10-453-372-542	Sequence 542, App	992	75	4.2	8746	7	US-11-098-686-10232	Sequence 10232, A
920	76.5	4.2	899	6	US-10-453-372-544	Sequence 544, App	993	74.5	4.1	107	7	US-11-185-615-2	Sequence 2, Appll
921	76.5	4.2	899	6	US-10-453-372-546	Sequence 546, App	994	74.5	4.1	109	7	US-11-056-186-3	Sequence 3, Appll
922	76.5	4.2	1124	7	US-11-049-536-162	Sequence 162, App	995	74.5	4.1	213	7	US-11-174-186-42	Sequence 42, Appll
923	76	4.2	110	7	US-11-193-512-33	Sequence 33, Appl	996	74.5	4.1	240	7	US-11-054-515-1391	Sequence 1391, Ap
924	76	4.2	144	7	US-11-055-163-15	Sequence 15, Appl	997	74.5	4.1	242	7	US-11-054-515-1884	Sequence 1884, Ap
925	76	4.2	238	7	US-11-054-515-2053	Sequence 2053, Ap	998	74.5	4.1	246	7	US-11-054-515-1264	Sequence 1264, Ap
926	76	4.2	249	7	US-11-054-515-2085	Sequence 2085, Ap	999	74.5	4.1	248	7	US-11-054-515-1363	Sequence 1363, Ap

1000	74.5	4.1	248	7	US-11-054-515-1388	Sequence 1388, Ap	1074	73.5	4.1	2228	7	US-11-124-367A-270	Sequence 270, App
1001	74.5	4.1	249	7	US-11-054-515-400	Sequence 400, App	1075	73.5	4.1	5712	7	US-11-143-980-47	Sequence 47, Appl
1002	74.5	4.1	249	7	US-11-054-515-417	Sequence 417, App	1076	73	4.0	107	7	US-11-004-590-330	Sequence 330, App
1003	74.5	4.1	249	7	US-11-054-515-448	Sequence 448, App	1077	73	4.0	218	7	US-11-004-590-229	Sequence 229, App
1004	74.5	4.1	249	7	US-11-054-515-683	Sequence 683, App	1078	73	4.0	238	7	US-11-054-515-1931	Sequence 1931, Ap
1005	74.5	4.1	251	7	US-11-054-515-286	Sequence 286, App	1079	73	4.0	239	7	US-11-054-515-2015	Sequence 2015, Ap
1006	74.5	4.1	251	7	US-11-054-515-1332	Sequence 1332, Ap	1080	73	4.0	240	7	US-11-054-515-1912	Sequence 1912, Ap
1007	74.5	4.1	251	7	US-11-054-515-3243	Sequence 3243, Ap	1081	73	4.0	245	7	US-11-054-515-1979	Sequence 1979, Ap
1008	74.5	4.1	259	7	US-11-054-515-1356	Sequence 1356, Ap	1082	73	4.0	247	7	US-11-054-515-1978	Sequence 1978, Ap
1009	74.5	4.1	311	7	US-11-000-463-817	Sequence 817, App	1083	73	4.0	249	7	US-11-054-515-1620	Sequence 1620, Ap
1010	74.5	4.1	459	6	US-10-935-494-5	Sequence 5, Appl	1084	73	4.0	251	7	US-11-054-515-1114	Sequence 1114, Ap
1011	74.5	4.1	470	7	US-11-144-248-46	Sequence 46, Appl	1085	73	4.0	251	7	US-11-054-515-1185	Sequence 1185, Ap
1012	74.5	4.1	470	7	US-11-144-222-46	Sequence 46, Appl	1086	73	4.0	255	7	US-11-054-515-1914	Sequence 1914, Ap
1013	74.5	4.1	470	7	US-11-182-343-46	Sequence 46, Appl	1087	73	4.0	256	7	US-11-054-515-1621	Sequence 1621, Ap
1014	74.5	4.1	1394	6	US-10-935-494-31	Sequence 31, Appl	1088	73	4.0	258	7	US-11-054-515-3246	Sequence 3246, Ap
1015	74	4.1	106	6	US-10-507-662-42	Sequence 42, Appl	1089	73	4.0	448	7	US-11-158-505-16	Sequence 16, Appl
1016	74	4.1	107	7	US-11-049-536-408	Sequence 408, App	1090	73	4.0	448	7	US-11-158-505-32	Sequence 32, Appl
1017	74	4.1	109	7	US-11-049-536-340	Sequence 340, App	1091	73	4.0	450	7	US-11-005-726-161	Sequence 161, Appl
1018	74	4.1	231	7	US-11-000-463-283	Sequence 283, App	1092	73	4.0	465	7	US-11-186-284-197	Sequence 197, App
1019	74	4.1	239	7	US-11-054-515-2035	Sequence 2035, Ap	1093	73	4.0	467	7	US-11-158-505-13	Sequence 13, Appl
1020	74	4.1	245	7	US-11-054-515-1477	Sequence 1477, Ap	1094	73	4.0	467	7	US-11-158-505-15	Sequence 15, Appl
1021	74	4.1	246	7	US-11-054-515-1314	Sequence 1314, Ap	1095	73	4.0	467	7	US-11-158-505-29	Sequence 29, Appl
1022	74	4.1	250	7	US-11-054-515-1952	Sequence 1952, Ap	1096	73	4.0	467	7	US-11-158-505-31	Sequence 31, Appl
1023	74	4.1	251	7	US-11-054-515-72	Sequence 72, Appl	1097	73	4.0	467	7	US-11-158-505-72	Sequence 72, Appl
1024	74	4.1	251	7	US-11-054-515-311	Sequence 311, App	1098	73	4.0	478	7	US-11-139-499-8	Sequence 8, Appl
1025	74	4.1	251	7	US-11-054-515-990	Sequence 990, App	1099	73	4.0	497	6	US-10-999-866-34	Sequence 34, Appl
1026	74	4.1	254	7	US-11-054-515-1186	Sequence 1186, Ap	1100	73	4.0	497	7	US-11-061-821-34	Sequence 34, Appl
1027	74	4.1	254	7	US-11-054-515-1196	Sequence 1196, Ap	1101	73	4.0	524	7	US-11-041-095-58	Sequence 58, Appl
1028	74	4.1	254	7	US-11-054-515-1673	Sequence 1673, Ap	1102	73	4.0	626	6	US-10-512-184-49	Sequence 49, Appl
1029	74	4.1	472	7	US-11-086-289-2	Sequence 2, Appl	1103	73	4.0	796	7	US-11-098-686-10187	Sequence 10187, A
1030	74	4.1	569	6	US-10-512-184-66	Sequence 66, Appl	1104	73	4.0	1881	7	US-11-040-473-8	Sequence 8, Appl
1031	74	4.1	883	6	US-10-793-626-754	Sequence 754, App	1105	73	4.0	2455	7	US-11-186-999-14	Sequence 14, Appl
1032	74	4.1	987	6	US-10-770-726-61	Sequence 61, Appl	1106	73	4.0	2455	7	US-11-186-999-16	Sequence 16, Appl
1033	74	4.1	1055	7	US-11-169-041-155	Sequence 155, App	1107	72.5	4.0	108	6	US-10-771-257-63	Sequence 63, Appl
1034	73.5	4.1	108	7	US-11-097-812-46	Sequence 46, Appl	1108	72.5	4.0	108	7	US-11-127-677-61	Sequence 61, Appl
1035	73.5	4.1	132	7	US-11-074-373-37	Sequence 37, Appl	1109	72.5	4.0	129	6	US-10-721-763-23	Sequence 23, Appl
1036	73.5	4.1	227	6	US-11-082-357-78	Sequence 78, Appl	1110	72.5	4.0	204	7	US-11-128-440-7	Sequence 7, Appl
1037	73.5	4.1	242	7	US-11-054-515-2046	Sequence 2046, Ap	1111	72.5	4.0	236	7	US-11-106-820-19	Sequence 19, Appl
1038	73.5	4.1	243	7	US-11-054-515-1929	Sequence 1929, Ap	1112	72.5	4.0	236	7	US-11-190-364-17	Sequence 17, Appl
1039	73.5	4.1	247	7	US-11-054-515-1193	Sequence 1193, Ap	1113	72.5	4.0	237	7	US-11-054-515-2039	Sequence 2039, Ap
1040	73.5	4.1	247	7	US-11-054-515-1294	Sequence 1294, Ap	1114	72.5	4.0	237	7	US-11-054-515-2112	Sequence 2112, Ap
1041	73.5	4.1	247	7	US-11-054-515-1294	Sequence 1296, Ap	1115	72.5	4.0	239	7	US-11-054-515-2034	Sequence 2034, Ap
1042	73.5	4.1	248	7	US-11-054-515-1465	Sequence 1465, Ap	1116	72.5	4.0	239	7	US-11-041-095-19	Sequence 19, Appl
1043	73.5	4.1	249	7	US-11-054-515-478	Sequence 478, App	1117	72.5	4.0	243	7	US-11-054-515-1916	Sequence 1916, Ap
1044	73.5	4.1	249	7	US-11-054-515-610	Sequence 610, App	1118	72.5	4.0	247	7	US-11-054-515-1322	Sequence 1322, Ap
1045	73.5	4.1	249	7	US-11-054-515-659	Sequence 659, App	1119	72.5	4.0	248	7	US-11-054-515-1246	Sequence 1246, Ap
1046	73.5	4.1	249	7	US-11-054-515-668	Sequence 668, App	1120	72.5	4.0	249	7	US-11-054-515-395	Sequence 395, App
1047	73.5	4.1	249	7	US-11-054-515-670	Sequence 670, App	1121	72.5	4.0	249	7	US-11-054-515-467	Sequence 467, App
1048	73.5	4.1	249	7	US-11-054-515-675	Sequence 675, App	1122	72.5	4.0	249	7	US-11-054-515-470	Sequence 470, App
1049	73.5	4.1	249	7	US-11-054-515-736	Sequence 736, App	1123	72.5	4.0	249	7	US-11-054-515-506	Sequence 506, App
1050	73.5	4.1	250	7	US-11-054-515-66	Sequence 66, Appl	1124	72.5	4.0	249	7	US-11-054-515-585	Sequence 585, App
1051	73.5	4.1	250	7	US-11-054-515-1851	Sequence 1851, Ap	1125	72.5	4.0	249	7	US-11-054-515-593	Sequence 593, App
1052	73.5	4.1	251	7	US-11-054-515-34	Sequence 34, Appl	1126	72.5	4.0	249	7	US-11-054-515-596	Sequence 596, App
1053	73.5	4.1	251	7	US-11-054-515-35	Sequence 35, Appl	1127	72.5	4.0	249	7	US-11-054-515-619	Sequence 619, App
1054	73.5	4.1	251	7	US-11-054-515-36	Sequence 36, Appl	1128	72.5	4.0	249	7	US-11-054-515-734	Sequence 734, App
1055	73.5	4.1	251	7	US-11-054-515-37	Sequence 37, Appl	1129	72.5	4.0	249	7	US-11-054-515-735	Sequence 735, App
1056	73.5	4.1	251	7	US-11-054-515-44	Sequence 44, Appl	1130	72.5	4.0	249	7	US-11-054-515-739	Sequence 739, App
1057	73.5	4.1	251	7	US-11-054-515-108	Sequence 108, App	1131	72.5	4.0	249	7	US-11-054-515-743	Sequence 743, App
1058	73.5	4.1	251	7	US-11-054-515-131	Sequence 131, App	1132	72.5	4.0	249	7	US-11-054-515-757	Sequence 757, App
1059	73.5	4.1	251	7	US-11-054-515-284	Sequence 284, App	1133	72.5	4.0	249	7	US-11-054-515-764	Sequence 764, App
1060	73.5	4.1	251	7	US-11-054-515-1049	Sequence 1049, Ap	1134	72.5	4.0	249	7	US-11-054-515-801	Sequence 801, App
1061	73.5	4.1	252	7	US-11-054-515-1495	Sequence 1495, Ap	1135	72.5	4.0	249	7	US-11-054-515-813	Sequence 813, App
1062	73.5	4.1	255	7	US-11-054-515-1608	Sequence 1608, Ap	1136	72.5	4.0	249	7	US-11-054-515-813	Sequence 813, App
1063	73.5	4.1	301	7	US-11-000-463-280	Sequence 280, App	1137	72.5	4.0	249	7	US-11-054-515-2002	Sequence 2002, Ap
1064	73.5	4.1	326	7	US-11-102-621-15	Sequence 15, Appl	1138	72.5	4.0	249	7	US-11-054-515-2033	Sequence 2033, Ap
1065	73.5	4.1	326	7	US-11-102-621-29	Sequence 29, Appl	1139	72.5	4.0	250	7	US-11-054-515-1616	Sequence 1616, Ap
1066	73.5	4.1	326	7	US-11-102-621-39	Sequence 39, Appl	1140	72.5	4.0	251	7	US-11-054-515-99	Sequence 99, Appl
1067	73.5	4.1	326	7	US-11-102-621-43	Sequence 43, Appl	1141	72.5	4.0	251	7	US-11-054-515-168	Sequence 168, Appl
1069	73.5	4.1	335	6	US-10-982-357-2	Sequence 2, Appl	1142	72.5	4.0	251	7	US-11-054-515-203	Sequence 203, App
1070	73.5	4.1	335	7	US-11-102-240-46	Sequence 46, Appl	1143	72.5	4.0	251	7	US-11-054-515-214	Sequence 214, App
1071	73.5	4.1	451	6	US-10-923-327-11	Sequence 11, Appl	1144	72.5	4.0	251	7	US-11-054-515-256	Sequence 256, App
1072	73.5	4.1	562	7	US-11-098-686-11416	Sequence 11416, A	1145	72.5	4.0	251	7	US-11-054-515-1045	Sequence 1045, Ap
1073	73.5	4.1	667	7	US-11-096-046-29	Sequence 29, Appl	1146	72.5	4.0	254	7		

1147	72.5	4.0	326	7	US-11-102-621-31	Sequence 31, Appl	1220	71.5	4.0	326	7	US-11-102-621-42	Sequence 42, Appl
1148	72.5	4.0	446	7	US-11-102-621-121	Sequence 121, App	1221	71.5	4.0	326	7	US-11-102-621-44	Sequence 44, Appl
1149	72.5	4.0	447	7	US-11-102-621-132	Sequence 132, App	1222	71.5	4.0	326	7	US-11-102-621-46	Sequence 46, Appl
1150	72.5	4.0	451	7	US-11-158-505-33	Sequence 33, Appl	1223	71.5	4.0	326	7	US-11-144-222-28	Sequence 28, Appl
1151	72.5	4.0	468	7	US-11-086-289-22	Sequence 22, Appl	1224	71.5	4.0	326	7	US-11-182-343-28	Sequence 28, Appl
1152	72.5	4.0	1047	6	US-10-510-386-200	Sequence 200, App	1225	71.5	4.0	326	7	US-11-124-620-2	Sequence 2, Appl
1153	72.5	4.0	1122	7	US-11-191-374-3	Sequence 3, Appl	1226	71.5	4.0	326	7	US-11-233-683-2	Sequence 2, Appl
1154	72.5	4.0	1122	7	US-11-191-375-3	Sequence 3, Appl	1227	71.5	4.0	411	6	US-10-453-372-74	Sequence 74, Appl
1155	72.5	4.0	1122	7	US-11-191-588-3	Sequence 3, Appl	1228	71.5	4.0	424	6	US-10-453-373-68	Sequence 68, Appl
1156	72.5	4.0	1479	7	US-11-019-711-36	Sequence 36, Appl	1229	71.5	4.0	442	7	US-11-102-621-124	Sequence 124, App
1157	72	4.0	107	7	US-11-004-590-257	Sequence 257, App	1230	71.5	4.0	442	7	US-11-102-621-125	Sequence 125, App
1158	72	4.0	107	7	US-11-004-590-329	Sequence 329, App	1231	71.5	4.0	442	7	US-11-102-621-127	Sequence 127, App
1159	72	4.0	234	7	US-11-041-095-25	Sequence 25, Appl	1232	71.5	4.0	442	7	US-11-102-621-128	Sequence 128, App
1160	72	4.0	244	7	US-11-054-515-1686	Sequence 1686, Ap	1233	71.5	4.0	446	7	US-11-102-621-138	Sequence 138, App
1161	72	4.0	247	7	US-11-054-515-1899	Sequence 1899, Ap	1234	71.5	4.0	577	7	US-11-082-389-134	Sequence 134, App
1162	72	4.0	247	7	US-11-054-515-2072	Sequence 2072, Ap	1235	71.5	4.0	579	7	US-11-174-186-41	Sequence 41, Appl
1163	72	4.0	248	7	US-11-054-515-920	Sequence 920, App	1236	71.5	4.0	589	6	US-10-763-712A-22	Sequence 22, Appl
1164	72	4.0	249	7	US-11-054-515-912	Sequence 912, App	1237	71.5	4.0	589	6	US-10-763-712A-98	Sequence 98, Appl
1165	72	4.0	249	7	US-11-054-515-1035	Sequence 1035, Ap	1239	71.5	4.0	854	7	US-11-022-562-219	Sequence 219, App
1166	72	4.0	251	7	US-11-054-515-955	Sequence 955, App	1240	71.5	4.0	997	7	US-11-080-991-519	Sequence 50, Appl
1167	72	4.0	251	7	US-11-054-515-1357	Sequence 1357, Ap	1241	71.5	4.0	999	7	US-11-113-424-36	Sequence 36, Appl
1168	72	4.0	251	7	US-11-054-515-1659	Sequence 1659, Ap	1242	71.5	4.0	2768	6	US-10-510-101-72	Sequence 72, Appl
1169	72	4.0	253	7	US-11-054-515-1650	Sequence 1650, Ap	1243	71	3.9	119	6	US-10-477-950-2	Sequence 2, Appl
1170	72	4.0	254	7	US-11-054-515-3	Sequence 3, Appl	1244	71	3.9	127	6	US-10-839-799-27	Sequence 27, Appl
1171	72	4.0	254	7	US-11-054-515-1288	Sequence 1288, Ap	1245	71	3.9	128	6	US-10-721-763-31	Sequence 31, Appl
1172	72	4.0	257	7	US-11-054-515-1531	Sequence 1531, Ap	1246	71	3.9	129	6	US-10-721-763-19	Sequence 19, Appl
1173	72	4.0	282	6	US-10-055-877-127	Sequence 127, App	1247	71	3.9	217	7	US-11-108-163B-13	Sequence 13, Appl
1174	72	4.0	282	7	US-11-087-177-9	Sequence 9, Appl	1248	71	3.9	220	7	US-11-108-163B-12	Sequence 12, Appl
1175	72	4.0	344	7	US-11-108-163B-10	Sequence 10, Appl	1249	71	3.9	240	7	US-11-054-515-2013	Sequence 2013, Ap
1176	72	4.0	346	7	US-11-221-203-14	Sequence 14, Appl	1250	71	3.9	243	7	US-11-054-515-2009	Sequence 2009, Ap
1177	72	4.0	409	7	US-11-113-424-73	Sequence 73, Appl	1251	71	3.9	246	7	US-11-054-515-1152	Sequence 1152, Ap
1178	72	4.0	444	7	US-11-004-590-233	Sequence 233, App	1252	71	3.9	247	7	US-11-054-515-924	Sequence 924, App
1179	72	4.0	503	7	US-11-113-424-72	Sequence 72, Appl	1253	71	3.9	249	7	US-11-054-515-1205	Sequence 1205, Ap
1180	72	4.0	539	7	US-11-183-136-38	Sequence 38, Appl	1254	71	3.9	249	7	US-11-054-515-1286	Sequence 1286, Ap
1181	72	4.0	570	7	US-11-113-424-69	Sequence 69, Appl	1255	71	3.9	249	7	US-11-054-515-1968	Sequence 1968, Ap
1182	72	4.0	570	7	US-11-113-424-71	Sequence 71, Appl	1256	71	3.9	251	7	US-11-054-515-1970	Sequence 1970, Ap
1183	72	4.0	620	7	US-11-113-424-70	Sequence 70, Appl	1257	71	3.9	251	7	US-11-054-515-943	Sequence 943, App
1184	72	4.0	627	6	US-10-493-909-47	Sequence 47, Appl	1258	71	3.9	251	7	US-11-054-515-1833	Sequence 1833, Ap
1185	72	4.0	667	7	US-11-096-046-28	Sequence 28, Appl	1259	71	3.9	253	7	US-11-054-515-929	Sequence 929, App
1186	72	4.0	667	7	US-11-096-046-30	Sequence 30, Appl	1260	71	3.9	253	7	US-11-054-515-935	Sequence 935, App
1187	72	4.0	695	7	US-11-096-046-26	Sequence 26, Appl	1261	71	3.9	253	7	US-11-054-515-939	Sequence 939, App
1188	72	4.0	720	7	US-11-113-424-28	Sequence 28, Appl	1262	71	3.9	253	7	US-11-054-515-1006	Sequence 1006, App
1189	72	4.0	747	7	US-11-113-424-26	Sequence 26, Appl	1263	71	3.9	254	7	US-11-054-515-1287	Sequence 1287, Ap
1190	72	4.0	898	6	US-10-453-372-522	Sequence 522, App	1264	71	3.9	254	7	US-11-054-515-1289	Sequence 1289, Ap
1191	72	4.0	2105	7	US-11-052-554A-173	Sequence 173, App	1265	71	3.9	256	7	US-11-054-515-839	Sequence 839, App
1192	72	4.0	2902	7	US-11-052-554A-91	Sequence 91, Appl	1266	71	3.9	301	7	US-11-108-163B-11	Sequence 11, Appl
1193	71.5	4.0	239	7	US-11-054-515-2023	Sequence 2023, Ap	1267	71	3.9	311	7	US-11-000-463-829	Sequence 829, App
1194	71.5	4.0	249	7	US-11-054-515-1400	Sequence 1400, Ap	1268	71	3.9	438	7	US-11-183-136-40	Sequence 40, Appl
1195	71.5	4.0	249	7	US-11-054-515-327	Sequence 327, App	1269	71	3.9	448	7	US-11-158-505-8	Sequence 8, Appl
1196	71.5	4.0	249	7	US-11-054-515-351	Sequence 351, App	1270	71	3.9	448	7	US-11-158-505-24	Sequence 24, Appl
1197	71.5	4.0	249	7	US-11-054-515-366	Sequence 366, App	1271	71	3.9	467	7	US-11-158-505-5	Sequence 5, Appl
1198	71.5	4.0	249	7	US-11-054-515-422	Sequence 422, App	1272	71	3.9	467	7	US-11-158-505-7	Sequence 7, Appl
1199	71.5	4.0	249	7	US-11-054-515-504	Sequence 504, App	1273	71	3.9	467	7	US-11-158-505-21	Sequence 21, Appl
1200	71.5	4.0	249	7	US-11-054-515-508	Sequence 508, App	1274	71	3.9	467	7	US-11-158-505-23	Sequence 23, Appl
1201	71.5	4.0	249	7	US-11-054-515-575	Sequence 575, App	1275	71	3.9	574	6	US-10-493-909-45	Sequence 45, Appl
1202	71.5	4.0	249	7	US-11-054-515-581	Sequence 581, App	1276	71	3.9	615	6	US-10-512-184-50	Sequence 50, Appl
1203	71.5	4.0	249	7	US-11-054-515-664	Sequence 664, App	1277	71	3.9	667	7	US-11-096-046-25	Sequence 25, Appl
1204	71.5	4.0	249	7	US-11-054-515-718	Sequence 718, App	1278	71	3.9	685	7	US-11-150-883-55	Sequence 55, Appl
1205	71.5	4.0	249	7	US-11-054-515-799	Sequence 799, App	1279	71	3.9	1268	7	US-11-150-883-54	Sequence 54, Appl
1206	71.5	4.0	252	7	US-11-054-515-1326	Sequence 1326, Ap	1280	71	3.9	2361	6	US-11-052-554A-1	Sequence 1, Appl
1207	71.5	4.0	252	7	US-11-054-515-1646	Sequence 1646, Ap	1281	71	3.9	2361	6	US-10-995-561-600	Sequence 600, App
1208	71.5	4.0	252	7	US-11-054-515-1821	Sequence 1821, Ap	1282	71	3.9	2361	6	US-10-511-545-1	Sequence 1, Appl
1209	71.5	4.0	254	7	US-11-054-515-977	Sequence 977, App	1283	71	3.9	2361	7	US-11-055-309A-9	Sequence 9, Appl
1210	71.5	4.0	326	6	US-10-999-866-36	Sequence 36, Appl	1284	71	3.9	2361	7	US-11-055-309A-10	Sequence 10, Appl
1211	71.5	4.0	326	6	US-10-493-909-22	Sequence 22, Appl	1285	70.5	3.9	213	7	US-11-172-320-4	Sequence 4, Appl
1212	71.5	4.0	326	7	US-11-144-248-28	Sequence 28, Appl	1286	70.5	3.9	213	7	US-11-173-969-4	Sequence 4, Appl
1213	71.5	4.0	326	7	US-11-061-821-36	Sequence 36, Appl	1287	70.5	3.9	241	7	US-11-054-515-1911	Sequence 1911, Ap
1214	71.5	4.0	326	7	US-11-102-621-10	Sequence 10, Appl	1288	70.5	3.9	243	7	US-11-054-515-1940	Sequence 1940, Ap
1215	71.5	4.0	326	7	US-11-102-621-32	Sequence 32, Appl	1289	70.5	3.9	248	7	US-11-054-515-861	Sequence 861, App
1216	71.5	4.0	326	7	US-11-102-621-35	Sequence 35, Appl	1290	70.5	3.9	248	7	US-11-054-515-1040	Sequence 1040, Ap
1217	71.5	4.0	326	7	US-11-102-621-37	Sequence 37, Appl	1291	70.5	3.9	248	7	US-11-054-515-1675	Sequence 1675, Ap
1218	71.5	4.0	326	7	US-11-102-621-40	Sequence 40, Appl	1292	70.5	3.9	248	7	US-11-054-515-1976	Sequence 1976, Ap
1219	71.5	4.0	326	7	US-11-102-621-41	Sequence 41, Appl	1293	70.5	3.9	248	7	US-11-054-515-2000	Sequence 2000, Ap

1294	70.5	3.9	248	7	US-11-054-515-2088	Sequence 2088, Ap	1367	70	3.9	258	7	US-11-054-515-1773	Sequence 1773, Ap
1295	70.5	3.9	249	7	US-11-054-515-346	Sequence 346, App	1368	70	3.9	274	7	US-11-195-739-7	Sequence 7, Appli
1296	70.5	3.9	249	7	US-11-054-515-362	Sequence 362, App	1369	70	3.9	694	7	US-11-074-176-340	Sequence 340, App
1297	70.5	3.9	249	7	US-11-054-515-388	Sequence 388, App	1370	70	3.9	697	7	US-11-074-176-150	Sequence 150, App
1298	70.5	3.9	249	7	US-11-054-515-420	Sequence 420, App	1371	70	3.9	833	6	US-10-453-372-518	Sequence 518, App
1299	70.5	3.9	249	7	US-11-054-515-499	Sequence 499, App	1372	70	3.9	1614	6	US-10-821-234-903	Sequence 903, App
1300	70.5	3.9	249	7	US-11-054-515-513	Sequence 513, App	1373	69.5	3.8	106	7	US-11-174-186-11	Sequence 11, Appl
1301	70.5	3.9	249	7	US-11-054-515-545	Sequence 545, App	1374	69.5	3.8	110	7	US-11-049-536-612	Sequence 612, App
1302	70.5	3.9	249	7	US-11-054-515-563	Sequence 563, App	1375	69.5	3.8	112	7	US-11-054-669-113	Sequence 113, App
1303	70.5	3.9	249	7	US-11-054-515-582	Sequence 582, App	1376	69.5	3.8	124	7	US-11-096-074-8	Sequence 8, Appli
1304	70.5	3.9	249	7	US-11-054-515-587	Sequence 587, App	1377	69.5	3.8	124	7	US-11-095-822-8	Sequence 8, Appli
1305	70.5	3.9	249	7	US-11-054-515-637	Sequence 637, App	1378	69.5	3.8	125	6	US-10-789-273-6	Sequence 6, Appli
1306	70.5	3.9	249	7	US-11-054-515-723	Sequence 723, App	1379	69.5	3.8	135	7	US-11-158-505-35	Sequence 35, Appl
1307	70.5	3.9	249	7	US-11-054-515-738	Sequence 738, App	1380	69.5	3.8	140	7	US-11-094-519A-48	Sequence 48, Appl
1308	70.5	3.9	249	7	US-11-054-515-746	Sequence 746, App	1381	69.5	3.8	215	6	US-10-374-954-9	Sequence 9, Appli
1309	70.5	3.9	249	7	US-11-054-515-753	Sequence 753, App	1382	69.5	3.8	227	6	US-10-982-357-77	Sequence 77, Appl
1310	70.5	3.9	249	7	US-11-054-515-1419	Sequence 1419, Ap	1383	69.5	3.8	229	6	US-10-858-730-85	Sequence 85, Appl
1311	70.5	3.9	249	7	US-11-054-515-1838	Sequence 1838, Ap	1384	69.5	3.8	232	7	US-11-000-463-343	Sequence 343, App
1312	70.5	3.9	250	7	US-11-054-515-1174	Sequence 1174, Ap	1385	69.5	3.8	233	7	US-11-128-900-15	Sequence 15, Appl
1313	70.5	3.9	250	7	US-11-054-515-1676	Sequence 1676, Ap	1386	69.5	3.8	233	7	US-11-128-900-67	Sequence 67, Appl
1314	70.5	3.9	251	7	US-11-054-515-1671	Sequence 1671, Ap	1387	69.5	3.8	235	7	US-11-128-900-14	Sequence 14, Appl
1315	70.5	3.9	253	7	US-11-054-515-938	Sequence 938, App	1388	69.5	3.8	235	7	US-11-128-900-65	Sequence 65, Appl
1316	70.5	3.9	253	7	US-11-054-515-1499	Sequence 1499, Ap	1389	69.5	3.8	236	7	US-11-144-248-48	Sequence 48, Appl
1317	70.5	3.9	254	7	US-11-054-515-838	Sequence 838, App	1390	69.5	3.8	236	7	US-11-144-222-48	Sequence 48, Appl
1318	70.5	3.9	264	7	US-11-176-525-1	Sequence 1, Appli	1391	69.5	3.8	236	7	US-11-182-343-48	Sequence 48, Appl
1319	70.5	3.9	326	7	US-11-102-621-16	Sequence 16, Appl	1392	69.5	3.8	241	7	US-11-054-515-1937	Sequence 1937, Ap
1320	70.5	3.9	326	7	US-11-102-621-30	Sequence 30, Appl	1393	69.5	3.8	243	7	US-11-054-515-1942	Sequence 1942, Ap
1321	70.5	3.9	326	7	US-11-102-621-33	Sequence 33, Appl	1394	69.5	3.8	244	7	US-11-054-515-1524	Sequence 1524, Ap
1322	70.5	3.9	326	7	US-11-102-621-38	Sequence 38, Appl	1395	69.5	3.8	247	7	US-11-054-515-996	Sequence 996, App
1323	70.5	3.9	326	7	US-11-102-621-45	Sequence 45, Appl	1396	69.5	3.8	247	7	US-11-054-515-1651	Sequence 1651, Ap
1324	70.5	3.9	326	7	US-11-102-621-47	Sequence 47, Appl	1397	69.5	3.8	247	7	US-11-054-515-1663	Sequence 1663, Ap
1325	70.5	3.9	429	7	US-11-098-686-11196	Sequence 1196, A	1398	69.5	3.8	247	7	US-11-054-515-1682	Sequence 1682, Ap
1326	70.5	3.9	429	7	US-11-124-368A-266	Sequence 266, App	1399	69.5	3.8	248	7	US-11-054-515-1718	Sequence 1718, Ap
1327	70.5	3.9	666	6	US-10-981-356A-27	Sequence 27, Appl	1400	69.5	3.8	248	7	US-11-054-515-1782	Sequence 1782, Ap
1328	70.5	3.9	666	6	US-10-981-356A-28	Sequence 28, Appl	1401	69.5	3.8	249	7	US-11-054-515-323	Sequence 323, App
1329	70.5	3.9	666	6	US-10-981-356A-30	Sequence 30, Appl	1402	69.5	3.8	249	7	US-11-054-515-335	Sequence 335, App
1330	70.5	3.9	666	7	US-11-096-046-27	Sequence 27, Appl	1403	69.5	3.8	249	7	US-11-054-515-336	Sequence 336, App
1331	70.5	3.9	692	6	US-10-981-356A-26	Sequence 26, Appl	1404	69.5	3.8	249	7	US-11-054-515-344	Sequence 344, App
1332	70.5	3.9	742	6	US-10-658-986-2	Sequence 2, Appli	1405	69.5	3.8	249	7	US-11-054-515-348	Sequence 348, App
1333	70.5	3.9	777	6	US-10-658-986-4	Sequence 4, Appli	1406	69.5	3.8	249	7	US-11-054-515-359	Sequence 359, App
1334	70.5	3.9	784	6	US-10-873-528-36	Sequence 36, Appl	1407	69.5	3.8	249	7	US-11-054-515-363	Sequence 363, App
1335	70.5	3.9	898	6	US-10-624-932-2	Sequence 2, Appli	1408	69.5	3.8	249	7	US-11-054-515-403	Sequence 403, App
1336	70.5	3.9	898	6	US-10-453-372-514	Sequence 514, App	1409	69.5	3.8	249	7	US-11-054-515-404	Sequence 404, App
1337	70.5	3.9	1041	6	US-10-828-831-9	Sequence 9, Appli	1410	69.5	3.8	249	7	US-11-054-515-414	Sequence 414, App
1338	70.5	3.9	1076	7	US-11-098-686-11184	Sequence 1184, A	1411	69.5	3.8	249	7	US-11-054-515-465	Sequence 465, App
1339	70	3.9	106	7	US-11-004-590-399	Sequence 399, App	1412	69.5	3.8	249	7	US-11-054-515-468	Sequence 468, App
1340	70	3.9	106	7	US-11-004-590-405	Sequence 405, App	1413	69.5	3.8	249	7	US-11-054-515-481	Sequence 481, App
1341	70	3.9	106	7	US-11-004-590-408	Sequence 408, App	1414	69.5	3.8	249	7	US-11-054-515-481	Sequence 515, App
1342	70	3.9	107	7	US-11-004-590-256	Sequence 256, App	1415	69.5	3.8	249	7	US-11-054-515-518	Sequence 518, App
1343	70	3.9	111	7	US-11-004-590-123	Sequence 123, App	1416	69.5	3.8	249	7	US-11-054-515-521	Sequence 521, App
1344	70	3.9	120	7	US-11-128-900-102	Sequence 102, App	1417	69.5	3.8	249	7	US-11-054-515-527	Sequence 527, App
1345	70	3.9	186	7	US-11-057-923-1	Sequence 1, Appli	1418	69.5	3.8	249	7	US-11-054-515-529	Sequence 529, App
1346	70	3.9	223	6	US-10-982-357-81	Sequence 81, Appli	1419	69.5	3.8	249	7	US-11-054-515-566	Sequence 566, App
1347	70	3.9	223	7	US-11-054-515-1947	Sequence 1947, Ap	1420	69.5	3.8	249	7	US-11-054-515-571	Sequence 571, App
1348	70	3.9	243	7	US-11-054-515-1972	Sequence 1972, Ap	1421	69.5	3.8	249	7	US-11-054-515-586	Sequence 586, App
1349	70	3.9	246	7	US-11-054-515-1589	Sequence 1589, Ap	1422	69.5	3.8	249	7	US-11-054-515-604	Sequence 604, App
1350	70	3.9	249	7	US-11-054-515-1199	Sequence 1199, Ap	1423	69.5	3.8	249	7	US-11-054-515-617	Sequence 617, App
1351	70	3.9	247	7	US-11-054-515-1443	Sequence 1443, Ap	1424	69.5	3.8	249	7	US-11-054-515-621	Sequence 621, App
1352	70	3.9	247	7	US-11-054-515-1704	Sequence 1704, Ap	1425	69.5	3.8	249	7	US-11-054-515-626	Sequence 626, App
1353	70	3.9	248	7	US-11-054-515-337	Sequence 337, App	1426	69.5	3.8	249	7	US-11-054-515-631	Sequence 631, App
1354	70	3.9	248	7	US-11-054-515-1476	Sequence 1476, Ap	1427	69.5	3.8	249	7	US-11-054-515-648	Sequence 648, App
1355	70	3.9	248	7	US-11-054-515-1653	Sequence 1653, Ap	1428	69.5	3.8	249	7	US-11-054-515-653	Sequence 653, App
1356	70	3.9	249	7	US-11-054-515-1109	Sequence 1109, Ap	1429	69.5	3.8	249	7	US-11-054-515-660	Sequence 660, App
1357	70	3.9	250	7	US-11-054-515-1191	Sequence 1191, Ap	1430	69.5	3.8	249	7	US-11-054-515-666	Sequence 666, App
1358	70	3.9	250	7	US-11-054-515-1797	Sequence 1797, Ap	1431	69.5	3.8	249	7	US-11-054-515-684	Sequence 684, App
1359	70	3.9	251	7	US-11-054-515-1411	Sequence 1411, Ap	1432	69.5	3.8	249	7	US-11-054-515-694	Sequence 694, App
1360	70	3.9	252	7	US-11-054-515-1695	Sequence 1695, Ap	1433	69.5	3.8	249	7	US-11-054-515-714	Sequence 714, App
1361	70	3.9	252	7	US-11-054-515-1192	Sequence 1192, Ap	1434	69.5	3.8	249	7	US-11-054-515-715	Sequence 715, App
1362	70	3.9	253	7	US-11-054-515-1199	Sequence 1199, Ap	1435	69.5	3.8	249	7	US-11-054-515-732	Sequence 732, App
1363	70	3.9	253	7	US-11-054-515-1200	Sequence 1200, Ap	1436	69.5	3.8	249	7	US-11-054-515-733	Sequence 733, App
1364	70	3.9	253	7	US-11-054-515-1353	Sequence 1353, Ap	1437	69.5	3.8	249	7	US-11-054-515-760	Sequence 760, App
1365	70	3.9	256	7	US-11-054-515-1301	Sequence 1301, Ap	1438	69.5	3.8	249	7	US-11-054-515-780	Sequence 780, App
1366	70	3.9	257	7	US-11-054-515-1327	Sequence 1327, Ap	1439	69.5	3.8	249	7	US-11-054-515-783	Sequence 783, App

1440	69.5	3.8	249	7	US-11-054-515-821	Sequence 821, App
1441	69.5	3.8	249	7	US-11-054-515-822	Sequence 822, App
1442	69.5	3.8	249	7	US-11-054-515-833	Sequence 833, App
1443	69.5	3.8	249	7	US-11-054-515-1335	Sequence 1335, Ap
1444	69.5	3.8	249	7	US-11-054-515-1724	Sequence 1724, Ap
1445	69.5	3.8	250	7	US-11-054-515-1348	Sequence 1348, Ap
1446	69.5	3.8	250	7	US-11-054-515-1484	Sequence 1484, Ap
1447	69.5	3.8	250	7	US-11-054-515-1977	Sequence 1977, Ap
1448	69.5	3.8	250	7	US-11-054-515-2066	Sequence 2066, Ap
1449	69.5	3.8	251	7	US-11-054-515-148	Sequence 148, App
1450	69.5	3.8	251	7	US-11-054-515-1317	Sequence 1317, Ap
1451	69.5	3.8	251	7	US-11-054-515-1390	Sequence 1390, Ap
1452	69.5	3.8	253	7	US-11-054-515-931	Sequence 931, App
1453	69.5	3.8	253	7	US-11-054-515-1364	Sequence 1364, Ap
1454	69.5	3.8	253	7	US-11-054-515-1814	Sequence 1814, Ap
1455	69.5	3.8	253	7	US-11-054-515-1858	Sequence 1858, Ap
1456	69.5	3.8	254	7	US-11-054-515-1195	Sequence 1195, Ap
1457	69.5	3.8	254	7	US-11-054-515-1428	Sequence 1428, Ap
1458	69.5	3.8	254	7	US-11-054-515-1544	Sequence 1544, Ap
1459	69.5	3.8	254	7	US-11-054-515-1735	Sequence 1735, Ap
1460	69.5	3.8	255	7	US-11-054-515-2087	Sequence 2087, Ap
1461	69.5	3.8	256	7	US-11-054-515-1745	Sequence 1745, Ap
1462	69.5	3.8	256	7	US-11-054-515-2080	Sequence 2080, Ap
1463	69.5	3.8	275	7	US-11-000-463-868	Sequence 868, App
1464	69.5	3.8	304	7	US-11-087-177-4	Sequence 4, Appli
1465	69.5	3.8	326	7	US-11-102-621-2	Sequence 2, Appli
1466	69.5	3.8	326	7	US-11-102-621-36	Sequence 36, Appl
1467	69.5	3.8	326	7	US-11-102-621-48	Sequence 48, Appl
1468	69.5	3.8	326	7	US-11-102-621-49	Sequence 49, Appl
1469	69.5	3.8	326	7	US-11-102-621-50	Sequence 50, Appl
1470	69.5	3.8	326	7	US-11-102-621-51	Sequence 51, Appl
1471	69.5	3.8	326	7	US-11-102-621-52	Sequence 52, Appl
1472	69.5	3.8	326	7	US-11-102-621-53	Sequence 53, Appl
1473	69.5	3.8	326	7	US-11-102-621-54	Sequence 54, Appl
1474	69.5	3.8	326	7	US-11-102-621-55	Sequence 55, Appl
1475	69.5	3.8	326	7	US-11-102-621-56	Sequence 56, Appl
1476	69.5	3.8	326	7	US-11-102-621-57	Sequence 57, Appl
1477	69.5	3.8	326	7	US-11-102-621-58	Sequence 58, Appl
1478	69.5	3.8	326	7	US-11-102-621-59	Sequence 59, Appl
1479	69.5	3.8	326	7	US-11-102-621-60	Sequence 60, Appl
1480	69.5	3.8	326	7	US-11-102-621-61	Sequence 61, Appl
1481	69.5	3.8	326	7	US-11-102-621-62	Sequence 62, Appl
1482	69.5	3.8	326	7	US-11-102-621-63	Sequence 63, Appl
1483	69.5	3.8	326	7	US-11-102-621-64	Sequence 64, Appl
1484	69.5	3.8	326	7	US-11-102-621-65	Sequence 65, Appl
1485	69.5	3.8	326	7	US-11-102-621-66	Sequence 66, Appl
1486	69.5	3.8	384	7	US-11-000-463-804	Sequence 804, App
1487	69.5	3.8	384	7	US-11-000-463-805	Sequence 805, App
1488	69.5	3.8	384	7	US-11-000-463-806	Sequence 806, App
1489	69.5	3.8	384	7	US-11-000-463-807	Sequence 807, App
1490	69.5	3.8	412	7	US-11-074-176-24	Sequence 24, Appl
1491	69.5	3.8	437	6	US-10-967-648A-4	Sequence 4, Appli
1492	69.5	3.8	439	7	US-11-198-819-12	Sequence 12, Appl
1493	69.5	3.8	446	7	US-11-102-621-119	Sequence 119, App
1494	69.5	3.8	446	7	US-11-102-621-120	Sequence 120, App
1495	69.5	3.8	446	7	US-11-102-621-122	Sequence 122, App
1496	69.5	3.8	446	7	US-11-102-621-123	Sequence 123, App
1497	69.5	3.8	447	7	US-11-102-621-130	Sequence 130, App
1498	69.5	3.8	447	7	US-11-102-621-131	Sequence 131, App
1499	69.5	3.8	447	7	US-11-102-621-133	Sequence 133, App
1500	69.5	3.8	447	7	US-11-102-621-134	Sequence 134, App

Search completed: February 15, 2006, 02:03:02
Job time : 28 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 7, 2006, 16:43:17 ; Search time 44 Seconds

(without alignments)
752.240 Million cell updates/sec

Title: US-09-981-915A-523

Perfect score: 1806

Sequence: 1 MKTIQKMHNSISWAIFTGL.....RRAGCVMLPLLVHLLKRP 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1639.5	90.8	344	2	156551
2	1285.5	71.2	338	2	JC1238
3	1268	70.2	345	2	JC4025
4	1266	70.1	345	2	S03199
5	1259	69.7	345	2	JC1239
6	936.5	51.9	338	2	JC5519
7	931.5	51.6	338	2	JC4776
8	297.5	16.5	333	2	A31923
9	283.5	15.7	725	1	IJMSNG
10	283.5	15.7	1115	1	IJMSNL
11	279.5	15.5	725	2	JE0099
12	279.5	15.5	1091	1	IJCHNL
13	278.5	15.4	4162	2	T42633
14	277.5	15.4	1088	1	IJXTNC
15	277.5	15.4	1088	1	IJXLNL
16	276	15.3	761	1	IJHUNG
17	275.5	15.3	853	1	IJBONC
18	273.5	15.1	725	2	JE0100
19	272.5	15.1	1323	2	PN0568
20	270.5	15.0	1092	1	JN0635
21	261.5	14.5	1091	2	S01998
22	259	14.3	7962	2	I38346
23	254.5	14.1	5175	2	T20992
24	254.5	14.1	5198	2	T43290
25	249.5	13.8	1040	2	A49356
26	246.5	13.6	1018	2	A54744
27	243.5	13.5	1021	2	A57112
28	243.5	13.5	1036	2	S22393
29	241.5	13.4	1018	2	JC4211

neuronal cell surf
heparan sulfate pr
hypothetical prote
axonal glycoprotei
hypothetical prote
CD22 homolog/B lym
kinase-like protei
protein UNC-89 - C
differentiation an
perlecan precursor
Down syndrome cell
fasciclin II precu
glial cell membran
dutt1 protein - mo
neuroglian - fruit
protein-tyrosine k
transmembrane rece
hypothetical prote
fasciclin II, tran
protein-tyrosine k
fasciclin II Pr-Li
protein-tyrosine k
plasmacytoma-asso
Big-1 protein - ra
neogenin - chicken
sax-3 protein - Ca
ror-related recept
nephin - human
B-cell adhesion pr
tumor suppressor p
hypothetical prote
myosin-light-chain
neurofascin - chic
frazzled gene prot
frazzled gene prot
neuronal cell adhesi
protein-tyrosine-p
probable neural ce
neuronal cell adhesi
neuronal cell adhesi
neural cell adhesi
CDO protein - rat
cell adhesion mole
cell adhesion mole
cell adhesion mole
neuronal cell adhesi
neuronal cell adhesi
hypothetical prote
CDO protein - huma
advanced glycosyla
carcinoembryonic a
rig-1 protein - mo
tumor suppressor -
myelin-associated
myelin-associated
cell adhesion prot
neuronal cell adhesi
hypothetical prote
hypothetical prote
Fit-1 tyrosine kin
myelin-associated
neuronal cell adhesi
receptor tyrosine
myelin-associated
telencephalin prec
hypothetical prote
Bravo/NR-CAM cell
fibroblast growth
hypothetical prote
KIAA992 protein -
hypothetical prote
projectin - fruit
titin, cardiac mus

103	173.5	9.6	1021	2	T42634	connectin/titin -	176	151	8.4	976	1	TVMSMD	macrophage colony-
104	172.5	9.6	264	2	T26976	hypothetical prote	177	151	8.4	1287	2	T30988	hypothetical prote
105	172.5	9.6	976	2	T29583	hypothetical prote	178	150.5	8.3	349	2	A34815	carcinoembryonic a
106	172.5	9.6	1800	2	T18531	tractin - medicina	179	150.5	8.3	824	2	S24108	protein-tyrosine k
107	172	9.5	286	2	A28333	carcinoembryonic a	180	150.5	8.3	1298	2	A48999	protein-tyrosine k
108	172	9.5	647	2	A35648	B-cell adhesion pr	181	150	8.3	769	2	S16236	fibroblast growth
109	171.5	9.5	1338	2	S09982	protein-tyrosine k	182	150	8.3	822	2	A45081	fibroblast growth
110	171	9.5	464	2	C30127	transmembrane carc	183	150	8.3	822	2	A41794	keratinocyte growt
111	171	9.5	526	1	A32164	biliary glycoprote	184	149.5	8.3	739	2	JS0675	vascular cell adhe
112	171	9.5	1257	1	A41060	neural cell adhesi	185	149.5	8.3	1501	2	S58148	protein-tyrosine-p
113	170	9.4	812	1	A36477	fibroblast growth	186	149.5	8.3	1863	2	S46217	protein-tyrosine-p
114	169	9.4	764	2	A49448	irregular chiasm C	187	149	8.3	335	2	H43354	pregnancy-specific
115	169	9.4	814	1	A39752	fibroblast growth	188	149	8.3	1894	2	CS4689	protein-tyrosine-p
116	168	9.3	1330	2	S49010	embryonic receptor	189	148.5	8.2	587	2	JH0464	DM-GRASP precursor
117	168	9.3	2051	2	T30938	receptor tyrosine	190	148.5	8.2	588	2	JH0506	adhesion molecule
118	168	9.3	2295	2	C88369	protein unc-52 [im	191	148.5	8.2	1907	2	S50893	protein-tyrosine-p
119	167.5	9.3	523	2	S50478	neurolin - goldfis	192	147.5	8.2	876	2	I49152	protein-tyrosine k
120	167.5	9.3	1694	2	S50065	sialoadhesin - mou	193	147.5	8.2	1499	2	I50212	protein-tyrosine-p
121	167	9.2	816	2	A49151	fibroblast growth	194	147	8.1	402	2	T09062	probable advanced
122	167	9.2	822	1	TVMSFG	fibroblast growth	195	147	8.1	406	2	E43354	pregnancy-specific
123	167	9.2	1356	2	JC1402	protein-tyrosine k	196	146.5	8.1	773	2	T46283	hypothetical prote
124	165.5	9.2	538	2	JC2457	vascular cell adhe	197	146	8.1	428	2	A27658	pregnancy-specific
125	165.5	9.2	646	2	I38049	cell surface glyco	198	146	8.1	852	2	I51259	tyrosine kinase C
126	165	9.1	584	2	T08678	hypothetical prote	199	146	8.1	1088	1	PFRTGA	platelet-derived g
127	165	9.1	822	2	I49289	fibroblast growth	200	146	8.1	1089	1	S33727	platelet-derived g
128	165	9.1	822	2	S29840	fibroblast growth	201	145.5	8.1	739	2	JN0581	vascular cell adhe
129	165	9.1	2222	2	T13924	adk protein - frui	202	145.5	8.1	799	2	S18209	fibroblast growth
130	164.5	9.1	583	2	I39428	alcam - human	203	145.5	8.1	1898	2	S46216	leukocyte antigen-
131	164.5	9.1	832	2	JH0393	fibroblast growth	204	145	8.0	972	1	TVHUMD	macrophage colony-
132	164	9.1	628	2	I38000	lutheran blood gro	205	144.5	8.0	1262	1	B48758	protein-tyrosine-p
133	163	9.0	818	2	T19120	hypothetical prote	206	144.5	8.0	1496	1	A48758	protein-tyrosine-p
134	162.5	9.0	1535	2	S46224	peroxidasin - frui	207	143.5	7.9	1177	2	T16594	hypothetical prote
135	162	9.0	321	2	JH0395	biliary glycoprote	208	143.5	7.9	13055	2	T16580	hypothetical prote
136	162	9.0	351	2	JH0396	biliary glycoprote	209	143	7.9	620	2	JH0593	hypothetical prote
137	162	9.0	417	2	JH0394	biliary glycoprote	210	143	7.9	687	2	A49636	Schwann cell myel
138	161	8.9	588	2	I37202	B-CAM protein - hu	211	143	7.9	1011	2	T13669	soluble vascular e
139	161	8.9	2541	2	T29340	hypothetical prote	212	142.5	7.9	326	2	F43354	neuromusculin - fr
140	160.5	8.9	980	1	TVCTMD	macrophage colony-	213	142.5	7.9	435	2	D33258	pregnancy-specific
141	160	8.9	622	1	C40862	heparin-binding gr	214	142.5	7.9	739	2	A41288	pregnancy-specific
142	160	8.9	822	1	TVHURF	fibroblast growth	215	142	7.9	806	2	A35963	vascular cell adhe
143	160	8.9	1437	2	T31093	probable protein-t	216	141.5	7.8	324	2	A43354	pregnancy-specific
144	160	8.9	6831	2	A88852	protein unc-22 [im	217	141.5	7.8	333	2	A43354	pregnancy-specific
145	160	8.9	6839	2	S57242	twitchin [similar]	218	141.5	7.8	789	2	T28714	hypothetical prote
146	158.5	8.8	1199	2	T32005	hypothetical prote	219	141.5	7.8	1227	2	T23004	hypothetical prote
147	158	8.7	351	2	PN0020	fibroblast growth	220	141.5	7.8	1355	2	T28715	hypothetical prote
148	158	8.7	822	2	B54846	fibroblast growth	221	141	7.8	254	2	C42691	fibroblast growth
149	157.5	8.7	941	1	TVVMVD	protein-tyrosine k	222	141	7.8	821	1	TVHUF2	fibroblast growth
150	157	8.7	239	2	S56749	junctional adhesio	223	140.5	7.8	397	2	C43354	pregnancy-specific
151	156.5	8.7	416	1	A42879	advanced glycosyla	224	140.5	7.8	705	2	S51635	fibroblast growth
152	156	8.6	978	2	S16385	macrophage colony-	225	140.5	7.8	823	2	B35963	protein-tyrosine k
153	156	8.6	7160	2	T27935	hypothetical prote	226	140.5	7.8	1089	1	PFHUGA	platelet-derived g
154	155.5	8.6	880	2	B53743	protein-tyrosine k	227	140	7.8	800	1	TVHUF2	fibroblast growth
155	155.5	8.6	1138	2	S24614	myosin-binding pro	228	140	7.8	800	2	A48991	heparin-binding gr
156	155	8.6	458	1	WMMSR1	biliary glycoprote	229	140	7.8	801	2	I55363	fibroblast growth
157	155	8.6	458	2	JC1509	biliary glycoprote	230	140	7.8	890	1	A53743	protein-tyrosine k
158	155	8.6	521	2	JC1508	biliary glycoprote	231	140	7.8	976	1	TVHUKT	protein-tyrosine k
159	155	8.6	521	2	S34338	biliary glycoprote	232	139.5	7.7	395	2	D43354	pregnancy-specific
160	155	8.6	1363	2	S58375	protein-tyrosine k	233	139.5	7.7	417	2	A28277	pregnancy-specific
161	155	8.6	1367	2	A41228	protein-tyrosine k	234	139.5	7.7	419	2	A33258	pregnancy-specific
162	154.5	8.6	602	2	A45769	acetylcholine rece	235	139.5	7.7	419	2	A31135	pregnancy-specific
163	154.5	8.6	1897	1	TDHULK	leukocyte antigen-	236	139.5	7.7	426	2	A35964	pregnancy-specific
164	154	8.5	1348	2	S51656	vascular endotheli	237	139.5	7.7	821	1	TVMSBK	fibroblast growth
165	153.5	8.5	588	2	A45254	surface glycoprote	238	139.5	7.7	1052	2	B43120	protein-tyrosine k
166	153	8.5	1912	2	A56178	protein-tyrosine-p	239	139	7.7	824	2	S36439	fibroblast growth
167	152.5	8.4	267	2	A38442	probable tumor sup	240	139	7.7	987	2	A88746	protein C18F3.2 [i
168	152.5	8.4	458	2	S23969	cell-adhesion mole	241	139	7.7	3488	2	T34418	hypothetical prote
169	152	8.4	525	1	A58674	neurotrophin-3 rec	242	138.5	7.7	413	2	S65948	hemolin - cecropia
170	152	8.4	803	1	S35695	neurotrophin-3 rec	243	138.5	7.7	426	2	B33258	pregnancy-specific
171	152	8.4	819	1	TVCHFG	fibroblast growth	244	138.5	7.7	426	2	A35341	pregnancy-specific
172	152	8.4	880	1	JC4166	protein-tyrosine k	245	138	7.6	1087	2	I51552	platelet-derived g
173	152	8.4	1123	2	S36846	myosin-binding pro	246	137.5	7.6	419	2	B54312	pregnancy-specific
174	151.5	8.4	344	2	A27681	nonspecific cross-	247	137.5	7.6	882	2	I38912	receptor tyrosine
175	151.5	8.4	422	2	S32357	glial growth facto	248	137.5	7.6	1379	2	JC4954	vascular endotheli

249	137	7.6	282	2	C28928	pregnancy-specific	322	134	6.9	436	2	B55181	pregnancy-specific
250	137	7.6	424	2	B36109	pregnancy-specific	323	134	6.9	495	2	A55181	pregnancy-specific
251	137	7.6	458	2	S68177	C-CAM2a protein is	324	134	6.9	650	1	JC1450	fibroblast growth
252	137	7.6	519	2	A44783	ecto-ATPase precu	325	124	6.9	999	2	I38547	novel cellular pro
253	137	7.6	524	2	S35341	ketin - fruit fly	326	124	6.9	1666	2	A48594	skelamin - mouse
254	136.5	7.6	738	2	A40096	platelet-endothell	327	123.5	6.8	402	2	A54312	pregnancy-specific
255	136.5	7.6	822	2	S19947	fibroblast growth	328	123.5	6.8	640	2	A43273	hergulin precurs
256	135.5	7.5	822	2	B49151	fibroblast growth	329	123	6.8	351	2	B34595	pregnancy-specific
257	135.5	7.5	975	2	T30816	macrophage colony-	330	123	6.8	476	1	A35104	brain-derived neur
258	134.5	7.4	419	2	JC4123	pregnancy-specific	331	123	6.8	821	1	S06943	myosin-light-chain
259	134.5	7.4	428	2	I57486	pregnancy-specific	332	123	6.8	1176	2	JN0583	neu differentiat
260	134.5	7.4	428	2	JS0032	pregnancy-specific	333	122.5	6.8	230	2	A58210	hergulin precurs
261	134.5	7.4	480	2	A56182	fibroblast growth	334	122.5	6.8	241	2	D43273	neu differentiat
262	134.5	7.4	647	2	B41288	vascular cell adhe	335	122.5	6.8	462	2	I38404	neu differentiat
263	134.5	7.4	729	2	A49120	fibroblast growth	336	122.5	6.8	636	2	I61718	neu differentiat
264	134	7.4	238	2	T22098	hypothetical prote	337	122.5	6.8	637	2	C43273	hergulin precurs
265	134	7.4	424	2	A34595	pregnancy-specific	338	122.5	6.8	639	2	I61719	neu differentiat
266	134	7.4	1147	2	A59307	myosin-light-chain	339	122.5	6.8	645	2	B43273	hergulin, aplice
267	133.5	7.4	888	2	S23065	ufo protein - mous	340	122.5	6.8	662	2	I61722	neu differentiat
268	133	7.4	336	2	C27658	pregnancy-specific	341	122	6.8	272	2	I48268	biliary glycoprote
269	133	7.4	413	2	A37778	hemolin precurs	342	122	6.8	850	2	JC5700	ErBB kinase activa
270	133	7.4	473	2	D88976	protein F54E2.4 li	343	121.5	6.7	332	2	JN0067	pregnancy-specific
271	133	7.4	612	2	I73633	gene trkC protein	344	121.5	6.7	365	2	JC7780	coxsackie- and ade
272	133	7.4	818	2	JC4058	fibroblast growth	345	121.5	6.7	365	2	JC7780	brain-derived neur
273	133	7.4	825	2	A55178	neurotrophin recep	346	121.5	6.7	474	1	C39667	brain-derived neur
274	133	7.4	839	1	I73632	neurotrophin-3 rec	347	121.5	6.7	520	1	S44099	brain-derived neur
275	132.5	7.3	275	2	B28928	pregnancy-specific	348	121.5	6.7	818	1	S44098	brain-derived neur
276	132.5	7.3	275	2	A28928	pregnancy-specific	349	121.5	6.7	821	1	A39667	brain-derived neur
277	132.5	7.3	584	2	I50419	s-glycerin precurs	350	121.5	6.7	1450	2	A44027	165K myofibrillar
278	132.5	7.3	856	2	I58411	protein-tyrosine k	351	121	6.7	292	2	T44044	glycoprotein [lmpo
279	132	7.3	1048	2	T30815	platelet-derived g	352	121	6.7	733	2	I49293	fibroblast growth
280	131.5	7.3	480	2	B56182	fibroblast growth	353	121	6.7	994	2	I49276	c-mer tyrosine kin
281	131.5	7.3	707	2	A38429	keratinocyte growt	354	121	6.7	1142	2	C33258	myosin-binding pro
282	131	7.3	439	2	S33766	platelet-derived g	355	120.5	6.7	212	2	C33258	pregnancy-specific
283	131	7.3	811	2	PN0889	connectin 1 - chic	356	120.5	6.7	353	2	S51242	heparin-binding fi
284	131	7.3	1106	1	PFHUGB	platelet-derived g	357	120.5	6.7	1742	2	S24600	projectin - fruit
285	130.5	7.2	310	2	JI0119	Fc gamma (IgG) rec	358	120	6.6	729	2	A56795	novel antigen rece
286	130.5	7.2	323	2	S06946	Fc gamma (IgG) rec	359	119.5	6.6	684	2	S60266	titin - rabbit (fr
287	130	7.2	802	1	TVHUP4	fibroblast growth	360	119.5	6.6	6805	2	S20901	neutrophil leucine-r
288	129.5	7.2	419	2	A36109	pregnancy-specific	361	119	6.6	707	2	JC7763	fibroblast growth
289	129.5	7.2	707	2	A54846	fibroblast growth	362	119	6.6	820	2	JI7295	fibroblast growth
290	129.5	7.2	1040	2	A57638	receptor tyrosine	363	119	6.6	860	2	JC5702	ErBB kinase activa
291	129.5	7.2	1103	2	T22889	hypothetical prote	364	119	6.6	868	2	JC5701	ErBB kinase activa
292	129	7.1	332	1	RWHUPD	poliovirus recepto	365	119	6.6	1274	2	S55050	cardiac myosin-bin
293	129	7.1	417	1	RMHUPA	poliovirus recepto	366	118	6.5	1451	2	S42167	190K protein - hum
294	129	7.1	1058	1	PFMSRB	platelet-derived g	367	117.5	6.5	182	2	I83053	pregnancy-specific
295	128.5	7.1	682	2	A35969	heparin-binding gr	368	117.5	6.5	335	2	A33514	pregnancy-specific
296	128	7.1	806	1	TVHUF3	glial growth facto	369	117.5	6.5	569	2	A36187	interleukin-1 rece
297	127.5	7.1	241	2	S23359	protein-tyrosine k	370	117.5	6.5	978	1	A49814	myosin-binding C-p
298	127	7.0	992	2	A39931	protein-tyrosine k	371	117	6.5	621	2	B57431	neutrophin-3 rec
299	126.5	7.0	592	2	S25705	Ig mu chain - shee	372	117	6.5	825	1	A40026	protein-tyrosine k
300	126.5	7.0	790	2	A39627	protein-tyrosine k	373	117	6.5	894	1	A41527	calcium vector pro
301	126	7.0	477	1	I73631	brain-derived neur	374	116.5	6.5	243	2	A37982	hypothetical prote
302	126	7.0	822	1	A56853	brain-derived neur	375	116.5	6.5	282	2	T17219	Fc gamma (IgG) rec
303	126	7.0	940	2	A40985	projectin - fruit	376	116.5	6.5	317	2	JI0118	hypothetical prote
304	126	7.0	1000	2	S18827	Flt3 protein - mou	377	116.5	6.5	599	2	T16774	hypothetical prote
305	125.5	6.9	251	2	T15495	hypothetical prote	378	116	6.4	253	2	T15475	hypothetical prote
306	125.5	6.9	278	2	JC1507	biliary glycoprote	379	116	6.4	268	2	T23555	hypothetical prote
307	125.5	6.9	335	2	B33251	nonspecific cross-	380	116	6.4	330	2	I46691	CD86 precursor - r
308	125.5	6.9	341	2	JC1511	biliary glycoprote	381	116	6.4	416	2	A54017	colon carcinoma-as
309	125.5	6.9	518	2	JC4024	poliovirus recepto	382	116	6.4	993	2	A36873	protein-tyrosine k
310	125.5	6.9	526	2	S70587	butyrophilin precu	383	115.5	6.4	526	2	A37821	butyrophilin - bov
311	125.5	6.9	975	1	TVMSKT	protein-tyrosine k	384	115.5	6.4	942	2	S23251	protein-tyrosine k
312	125	6.9	278	2	JC1506	biliary glycoprote	385	115	6.4	166	2	A33402	pregnancy-specific
313	125	6.9	341	2	JC1512	biliary glycoprote	386	115	6.4	813	1	A49123	fibroblast growth
314	125	6.9	977	2	I45877	protein-tyrosine k	387	115	6.4	1462	1	B36182	protein-tyrosine-p
315	124.5	6.9	750	2	S41051	fibroblast growth	388	114.5	6.3	326	2	JC4124	pregnancy-specific
316	124.5	6.9	829	2	JC4583	fibroblast growth	389	114	6.3	302	2	C36464	fibroblast growth
317	124.5	6.9	960	1	JN0877	protein-tyrosine k	390	114	6.3	432	1	RMQOT4	T-cell surface gly
318	124	6.9	278	2	A39037	carcinoembryonic a	391	114	6.3	713	2	I50128	unc-5 protein, lon
319	124	6.9	426	2	C55181	pregnancy-specific	392	114	6.3	947	1	B44294	myosin-binding pro
320	124	6.9	426	2	S09016	pregnancy-specific	393	114	6.3	1132	2	A35089	Fc gamma (IgG) rec
321	124	6.9	426	2	B35334	pregnancy-specific	394	113.5	6.3	344	2	A41357	

395	113.5	6.3	374	1	A39878	Fc gamma (IgG) rec	468	100	5.5	395	2	T05906	probable polygalac
396	113.5	6.3	547	1	S28904	intercellular adhe	469	100	5.5	531	2	S08016	intercellular adhe
397	113.5	6.3	1465	2	S43529	165K protein, skel	470	100	5.5	537	2	I49769	intercellular adhe
398	113	6.3	530	2	A53437	poliovirus recepto	471	100	5.5	641	2	D71170	hypothetical prote
399	112.5	6.2	304	1	RWCHH7	cell surface glyco	472	99	5.5	537	2	A45815	intercellular adhe
400	112.5	6.2	503	2	JC5287	SHP substrate-1 pr	473	99	5.5	869	2	T44440	chitinase (EC 3.2.
401	112.5	6.2	666	2	H89581	protein din-1 lim	474	99	5.5	1160	2	F88369	protein unc-52 [im
402	112.5	6.2	954	2	I51703	c-kit-related kina	475	98.5	5.5	629	2	A48500	ly-9.2 antigen - m
403	112.5	6.2	2109	2	E89066	protein H05009.1 [476	98	5.5	238	2	A49633	Ig lambda-like cha
404	112.5	6.2	2109	2	T33247	hypothetical prote	477	98	5.4	524	2	JQ0683	type-specific anti
405	112	6.2	573	2	S12838	Ig mu chain precu	478	98	5.4	544	2	JC5018	intercellular adhe
406	112	6.2	1327	2	T09402	immunoglobulin-lik	479	98	5.4	773	1	QRRBG	secretory componen
407	111.5	6.2	335	2	C54312	pregnancy-specific	480	98	5.4	1000	2	I46521	titin - rabbit (fr
408	111.5	6.2	392	2	B44194	poliovirus recepto	481	97.5	5.4	197	2	PQ0327	heparin-binding fi
409	111.5	6.2	417	2	A44194	poliovirus recepto	482	97.5	5.4	270	2	S65739	basigin precursor
410	111.5	6.2	567	2	S29498	lymphocyte antigen	483	97	5.4	172	2	B26414	95K nonspecific cr
411	111	6.1	210	2	JC4122	hypothetical prote	484	97	5.4	465	2	B97235	deacetylase/dipep
412	111	6.1	292	2	T44230	pregnancy-specific	485	97	5.4	874	2	T29548	hypothetical prote
413	111	6.1	398	2	S17428	interleukin-1 rece	486	96.5	5.3	309	2	I49503	B-lymphocyte activ
414	111	6.1	748	2	S41050	fibroblast growth	487	96.5	5.3	364	2	T46926	hypothetical prote
415	110.5	6.1	509	2	JC5288	SHP substrate-1 pr	488	96.5	5.3	437	2	A64488	hypothetical prote
416	110.5	6.1	513	2	JC5289	SHP substrate-1 pr	489	96.5	5.3	475	2	I76668	pregnancy-specific
417	110	6.1	285	2	S36903	Fc gamma (IgG) rec	490	96.5	5.3	580	2	A46538	Ig heavy chain, se
418	110	6.1	508	2	A33378	fasciclin III prec	491	96.5	5.3	709	2	A35364	carcinoembryonic a
419	110	6.1	919	2	T32541	unc-5 protein - Ca	492	96	5.3	455	1	MHMS	Ig mu chain C regi
420	110	6.1	1579	2	B91290	probable invasin [493	96	5.3	455	2	A24976	Ig mu chain C regi
421	110	6.1	1700	2	G86131	probable invasin Z	494	96	5.3	476	1	MHMSM	Ig mu chain C regi
422	109.5	6.1	164	2	T19795	hypothetical prote	495	96	5.3	562	2	G02426	interleukin-1 rece
423	109.5	6.1	196	2	T19794	hypothetical prote	496	96	5.3	790	1	TVHUTT	nerve growth facto
424	109.5	6.1	206	2	A40305	biliary glycoprote	497	95.5	5.3	309	2	S15674	cell surface glyco
425	109.5	6.1	470	2	S22080	Ig heavy chain pre	498	95.5	5.3	330	2	A29915	teratocarcinoma gl
426	109.5	6.1	532	1	A29849	intercellular adhe	499	95.5	5.3	345	2	A46052	vascular cell adhe
427	108	6.0	207	2	A56190	titin - rat (fragm	500	95.5	5.3	375	2	I60125	PDGF receptor beta
428	108	6.0	267	2	I72882	Fc gamma receptor	501	95	5.3	267	2	A35902	Fc gamma (IgG) rec
429	108	6.0	467	1	HLMSP3	poliovirus recepto	502	95	5.3	277	2	I52825	gene MAC25 protein
430	108	6.0	474	1	OMHU1B	alpha-1-B-glycopro	503	95	5.3	282	2	S50031	prostatcyclin-stimu
431	107.5	6.0	352	2	I77374	pregnancy-specific	504	95	5.3	329	2	A44065	fibroblast growth
432	107.5	6.0	404	2	A46480	Fc gamma (IgG) rec	505	95	5.3	799	1	TVRTTB	nerve growth facto
433	107.5	6.0	537	2	A46611	myosin-binding pro	506	95	5.3	3283	2	AC1018	large repetitive p
434	106.5	5.9	336	2	A42632	Fit-1S protein pre	507	94.5	5.2	182	2	A34647	pregnancy-specific
435	106.5	5.9	367	1	MHCH	Ig mu chain C regi	508	94.5	5.2	355	2	D72174	D9R protein - vari
436	106	5.9	407	2	T08732	hypothetical prote	509	94.5	5.2	1184	2	T09484	cartilage intermed
437	105.5	5.8	326	2	T37450	interleukin-1 beta	510	94.5	5.2	1280	2	AB1981	hypothetical prote
438	105.5	5.8	487	2	T28804	hypothetical prote	511	94.5	5.2	1452	1	S17670	protein-tyrosine-p
439	105	5.8	131	2	T20334	hypothetical prote	512	94.5	5.2	2347	1	TVHURS	kinase-related pro
440	105	5.8	269	2	A45506	leukocyte activati	513	94	5.2	328	2	I47159	Ig gamma 2a chain
441	104.5	5.8	220	2	F42527	B16R protein - vac	514	94	5.2	757	2	I45956	polymERIC immunogl
442	104	5.8	1471	2	T19506	hypothetical prote	515	93.5	5.2	194	2	T29925	hypothetical prote
443	103.5	5.7	240	2	JC4121	pregnancy-specific	516	93.5	5.2	265	2	A55811	hypothetical prote
444	103.5	5.7	326	1	WNV215	B15R protein precu	517	93.5	5.2	354	2	S46877	B20R protein - var
445	103.5	5.7	487	2	S65133	butyrophilin - mou	518	93.5	5.2	354	2	T28616	hypothetical prote
446	103.5	5.7	531	2	S20900	titin - mouse (fra	519	93.5	5.2	1366	2	B84924	colorectal cancer
447	103.5	5.7	538	2	I68093	PRR2 delta - human	520	93	5.1	144	2	B40098	hypothetical prote
448	103	5.7	618	2	T08685	hypothetical prote	521	93	5.1	267	2	I56110	Fc-gamma RIIB-alp
449	103	5.7	943	2	B45082	neutrophilic recep	522	93	5.1	299	2	I46690	CD80 precursor - r
450	102.5	5.7	237	2	S00882	IgE Fc receptor al	523	93	5.1	352	2	T33433	hypothetical prote
451	102.5	5.7	336	2	I48471	Fc gamma (IgG) rec	524	93	5.1	393	2	S16844	hypothetical prote
452	102.5	5.7	1021	2	I39207	leukocyte surface	525	92.5	5.1	213	2	JE0247	colorectal cancer
453	102	5.6	351	1	SAV2VW	surface antigen pr	526	92.5	5.1	274	2	T32736	translation elonga
454	102	5.6	478	2	I53960	PRR2 alpha - human	527	92.5	5.1	298	2	H64247	interleukin 1 rece
455	102	5.6	1398	2	T25568	hypothetical prote	528	92.5	5.1	590	2	I56526	hypothetical prote
456	101.5	5.6	275	2	JC7604	CD86 spliced varia	529	92.5	5.1	1220	2	T32916	Ig gamma 2b chain
457	101.5	5.6	329	1	A48754	B7-2 antigen - hum	530	92	5.1	328	2	I47160	Ig gamma 2b chain
458	101.5	5.6	625	2	T16777	hypothetical prote	531	92	5.1	460	2	JC2194	vasoactive intest1
459	101.5	5.6	937	2	A45082	neutrophilic recep	532	92	5.1	545	2	HU0341	intercellular adhe
460	101	5.6	351	1	SAV2MR	surface antigen pr	533	91.5	5.1	455	2	J96797	hypothetical prote
461	101	5.6	353	1	SAV2VC	hypothetical prote	534	91	5.0	132	2	S14077	Ig kappa chain - A
462	101	5.6	421	2	T46266	hypothetical prote	535	91	5.0	370	2	A96741	hypothetical prote
463	101	5.6	458	1	RWHU74	T-cell surface gly	536	91	5.0	416	2	S33473	interleukin-1 rece
464	101	5.6	751	2	I48748	semaphorin E - mou	537	91	5.0	427	2	G02034	killer cell inhibi
465	100.5	5.6	274	2	A47639	OX-2 membrane glyc	538	90.5	5.0	391	2	T09058	butyrophilin homol
466	100	5.5	235	2	S20000	Ig light chain pre	539	90.5	5.0	1269	2	F90538	hypothetical prote
467	100	5.5	304	2	B88746	protein C18F3.3 [i	540	90	5.0	283	1	FCMSG1	Fc gamma (IgG) rec

541	90	5.0	236	2	I46021	Fc-gamma receptor	614	85	4.7	1526	2	T19473	hypothetical prote
542	90	5.0	432	1	RWCZT4	T-cell surface gly	615	85	4.7	2274	2	T30258	adenomatous polyo
543	90	5.0	444	2	G01924	KIR (cl-2) NK rece	616	85	4.7	2339	2	S41121	acetyl-CoA carboxy
544	90	5.0	576	2	A32604	interleukin-1 rece	617	85	4.7	4351	2	T00252	MEGF1 protein - ra
545	90	5.0	721	2	C82939	virulence associat	618	84.5	4.7	240	2	S01299	OX-45 membrane gly
546	90	5.0	858	1	VCLJG2	env polypeptin pr	619	84.5	4.7	243	2	A53244	leukocyte antigen
547	90	5.0	1357	2	T29265	hypothetical prote	620	84.5	4.7	330	2	A40071	Fc gamma (IgG) rec
548	90	5.0	1282	2	T42717	DNA-binding prote	621	84.5	4.7	330	2	I49660	Fc gamma-1/gamma-2
549	89.5	5.0	131	2	F45893	T-cell receptor al	622	84.5	4.7	385	2	T01332	hypothetical prote
550	89.5	5.0	245	2	A30154	IgE receptor alpha	623	84.5	4.7	466	2	AF0172	asparagine-cRNA li
551	89.5	5.0	254	1	JL0107	Fc gamma (IgG) rec	624	84.5	4.7	727	2	S54512	hypothetical prote
552	89.5	5.0	362	2	A56745	microfibril-associ	625	84.5	4.7	897	2	E65127	Probable bifunctio
553	89.5	5.0	1134	1	JN0711	protein-tyrosine k	626	84.5	4.7	1133	2	T01757	hypothetical prote
554	89.5	5.0	1691	1	D54689	protein-tyrosine-p	627	84.5	4.7	1227	2	T48028	hypothetical prote
555	89	4.9	257	2	PS0401	basigin type II -	628	84	4.7	136	1	KVM321	Ig kappa chain pre
556	89	4.9	271	2	S43512	GP42/Basigin prote	629	84	4.7	162	2	I51668	tumor suppressor -
557	89	4.9	273	2	JK0107	basigin precursor	630	84	4.7	225	2	G89936	conserved hypothet
558	89	4.9	275	2	PS0402	basigin type III -	631	84	4.7	240	2	JL0143	antigen BCM1 precu
559	89	4.9	429	1	EHRT	Ig epsilon chain C	632	84	4.7	246	2	A29523	T-cell surface gly
560	89	4.9	598	2	A57249	beta-galactosidase	633	84	4.7	337	2	AG0963	hypothetical prote
561	89	4.9	769	1	ORRTGS	secretory componen	634	84	4.7	466	2	JC5897	killer cell inhibi
562	89	4.9	1452	1	S17669	protein-tyrosine-p	635	84	4.7	495	2	JC2195	vasoactive intesti
563	88.5	4.9	309	2	I49522	gene B7-2 protein	636	84	4.7	737	2	I39547	S-protein secretio
564	88	4.9	331	2	T15587	hypothetical prote	637	84	4.7	997	2	D75012	hypothetical prote
565	88	4.9	757	1	S48841	secretory componen	638	84	4.7	1442	2	S72441	protein-tyrosine-p
566	88	4.9	832	2	AD1096	internalin protein	639	84	4.7	1477	2	B43855	high-molecular-wei
567	88	4.9	4436	2	E71086	hypothetical prote	640	84	4.7	1536	2	A43855	high-molecular-wei
568	87.5	4.8	151	2	T31607	hypothetical prote	641	83.5	4.6	110	2	B30583	T-cell receptor de
569	87.5	4.8	280	2	I55577	Fc gamma (IgG) rec	642	83.5	4.6	134	2	S21917	Ig kappa chain V r
570	87.5	4.8	321	2	I54766	B-lymphocyte activ	643	83.5	4.6	245	2	T07071	beta-fructofuranos
571	87.5	4.8	368	2	S17980	pgai protein - Asp	644	83.5	4.6	315	1	HNW24X	hemagglutinin prec
572	87.5	4.8	402	2	T29703	hypothetical prote	645	83.5	4.6	328	2	S30444	Str2 protein - huma
573	87.5	4.8	660	2	H71376	probable tpr prote	646	83.5	4.6	374	2	S69339	Ig heavy chain V r
574	87	4.8	359	2	A97175	undecaprenyl-PP-Mu	647	83.5	4.6	405	1	B42606	cytochrome P450 CV
575	87	4.8	383	2	T21946	hypothetical prote	648	83.5	4.6	490	2	B96952	sucrase-6-phosphat
576	87	4.8	477	2	B64115	asparagine-tRNA li	649	83.5	4.6	513	2	F86320	hypothetical prote
577	87	4.8	814	2	I40048	S-layer protein pr	650	83.5	4.6	583	2	S57721	cepB protein - Clo
578	87	4.8	974	1	A49714	protein-tyrosine k	651	83.5	4.6	1054	2	T18304	acid trehalase hom
579	87	4.8	2458	2	T17420	probable polyketid	652	83.5	4.6	1657	2	T25421	hypothetical prote
580	86.5	4.8	235	2	S25058	Ig kappa chain - m	653	83	4.6	220	2	A49444	Ig gamma-1 heavy c
581	86.5	4.8	278	1	TDRTOX	OX-2 membrane gly	654	83	4.6	313	2	JQ1862	3ir protein - vari
582	86.5	4.8	440	2	D71715	hypothetical prote	655	83	4.6	315	1	HNWZV	hemagglutinin prec
583	86.5	4.8	1533	2	T00344	hypothetical prote	656	83	4.6	410	2	C69197	ATP-dependent 26S
584	86	4.8	387	2	T04320	polysaccharuronase	657	83	4.6	555	2	JQ1526	interleukin-1 rece
585	86	4.8	387	2	T07591	polysaccharuronase	658	83	4.6	563	2	C95874	conserved hypothet
586	86	4.8	444	2	G01925	KIR (cl-11) NK rec	659	83	4.6	630	2	AE2312	transketolase (imp
587	86	4.8	501	1	A60005	glycoprotein A pre	660	83	4.6	680	2	JC5895	killer cell inhibi
588	86	4.8	501	1	VBEMBA	glycoprotein A pre	661	83	4.6	767	2	S41479	DNA-binding protei
589	86	4.8	501	1	VBEMBA	glycoprotein A pre	662	83	4.6	1014	2	T24412	hypothetical prote
590	86	4.8	505	1	VBEMH	glycoprotein gp57-	663	83	4.6	1033	2	A12359	hypothetical prote
591	86	4.8	580	2	A96883	hypothetical prote	664	83	4.6	2638	1	A42545	genome polypeptin
592	86	4.8	587	2	S36231	beta-fructofuranos	665	83	4.6	4836	2	T14346	huc2 protein - mo
593	86	4.8	856	1	A44963	env polypeptin pr	666	82.5	4.6	125	2	A53627	fibroblast growth
594	86	4.8	1394	2	S60762	IgA-specific serin	667	82.5	4.6	160	2	I47163	cytolitic trigger
595	86	4.8	1711	2	AB1283	peptidoglycan link	668	82.5	4.6	197	2	S29593	Ig kappa chain (WM
596	85.5	4.7	475	2	A54879	pregnancy-specific	669	82.5	4.6	233	2	JC5322	p53 specific singl
597	85.5	4.7	510	2	FC4054	cardiac C-protein	670	82.5	4.6	247	1	RMW372	T-cell surface gly
598	85.5	4.7	593	1	DTCHPH	purH bifunctional	671	82.5	4.6	315	2	T37438	hemagglutinin - va
599	85.5	4.7	764	1	QRHUGS	secretory componen	672	82.5	4.6	429	2	T36088	probable secreted
600	85.5	4.7	1145	1	GNLJEV	HIV-1 retropepsin	673	82.5	4.6	433	2	S31436	Ig upsilon chain -
601	85.5	4.7	1146	1	GNLJ22	HIV-1 retropepsin	674	82.5	4.6	610	2	T25262	hypothetical prote
602	85.5	4.7	1146	1	GNLJEW	HIV-1 retropepsin	675	82.5	4.6	871	2	H81430	translatation initia
603	85.5	4.7	1732	2	T30836	lysine-specific cy	676	82.5	4.6	1553	2	T18502	hypothetical prote
604	85	4.7	505	2	B84831	hypothetical prote	677	82	4.5	120	2	D29775	Ig kappa chain pre
605	85	4.7	635	2	JC5896	killer cell inhibi	678	82	4.5	225	2	I51335	Ig lambda chain -
606	85	4.7	753	2	B32628	platelet glycoprot	679	82	4.5	230	2	S49449	Ig lambda chain -
607	85	4.7	778	2	A60798	platelet glycoprot	680	82	4.5	270	2	A34636	B-cell-restricted
608	85	4.7	788	2	A26547	platelet glycoprot	681	82	4.5	288	2	A45803	hemagglutinin - va
609	85	4.7	788	2	T77349	platelet glycoprot	682	82	4.5	313	2	H36854	K9R protein - vari
610	85	4.7	817	2	A48721	titin, muscle - ch	683	82	4.5	318	2	F72171	glycoprotein A - t
611	85	4.7	832	2	E71492	hypothetical prote	684	82	4.5	489	1	VBETA	glycoprotein gp57-
612	85	4.7	939	2	I41197	eae protein (enter	685	82	4.5	523	1	A60408	hypothetical prote
613	85	4.7	1436	2	JC5290	protein-tyrosine-p	686	82	4.5	630	2	T38637	

687	82	4.5	663	1	OREGIC	colicin I receptor	760	79.5	4.4	290	2	C97533	pyruvate dehydroge
688	82	4.5	820	2	T14879	hypothetical prote	761	79.5	4.4	306	2	AE2752	pyruvate dehydroge
689	82	4.5	841	2	JCS594	killer cell inhibi	762	79.5	4.4	468	1	A41242	interleukin-6 rece
690	82	4.5	842	2	T04555	hypothetical prote	763	79.5	4.4	474	2	I50830	Ig mu chain - Iepi
691	82	4.5	1125	1	S57846	hypothetical prote	764	79.5	4.4	522	2	B42804	immunodominant typ
692	82	4.5	1222	2	T22490	hypothetical prote	765	79.5	4.4	558	2	A44964	apical membrane an
693	82	4.5	1577	2	T30858	glucosyltransferas	766	79.5	4.4	653	2	A49722	endoglin precursor
694	81.5	4.5	107	2	PL0268	Ig kappa chain v r	767	79.5	4.4	722	1	CDHU26	dipeptidyl-peptida
695	81.5	4.5	240	2	A41797	Ig light chain - s	768	79.5	4.4	1022	1	S00503	Na+/K+-exchanging
696	81.5	4.5	247	2	A34954	ST2v protein - hum	769	79.5	4.4	1034	1	A53663	enteropeptidase (E
697	81.5	4.5	259	2	JC7109	T-cell surface gly	770	79.5	4.4	1036	2	B69368	hypothetical prote
698	81.5	4.5	656	2	T23338	hypothetical prote	771	79.5	4.4	1156	2	T23308	hypothetical prote
699	81.5	4.5	1183	2	A89135	protein F2566.2 li	772	79.5	4.4	1185	2	A42404	collagen adhesin -
700	81.5	4.5	1203	2	S27545	pullulanase - ther	773	79.5	4.4	1409	2	T42522	protein-tyrosine-p
701	81.5	4.5	1336	2	T17479	hypothetical prote	774	79.5	4.4	1422	2	T30111	hypothetical prote
702	81.5	4.5	1963	2	G86643	hypothetical prote	775	79	4.4	91	2	S17638	Ig kappa chain v r
703	81	4.5	234	2	S14237	Ig kappa chain pre	776	79	4.4	101	2	H37262	Ig heavy chain v r
704	81	4.5	247	2	A55717	myelin/oligodendro	777	79	4.4	231	2	S25753	Ig lambda chain -
705	81	4.5	314	1	HNV2VM	hemagglutinin prec	778	79	4.4	348	2	C81284	cystathionine beta
706	81	4.5	314	1	JQ1793	hemagglutinin prec	779	79	4.4	370	2	G97001	endoglucanase fami
707	81	4.5	451	2	S71754	cellular hepatitis	780	79	4.4	387	2	T04322	polysialacturonase
708	81	4.5	545	2	A38447	oligopeptide ABC t	781	79	4.4	403	2	T20727	hypothetical prote
709	81	4.5	568	2	A45804	Ig mu chain C regi	782	79	4.4	432	2	S30193	T-cell surface gly
710	81	4.5	571	2	H69584	acetolactate synth	783	79	4.4	450	2	B97292	probable ATP-depen
711	81	4.5	578	2	B96683	hypothetical prote	784	79	4.4	474	1	G2MS11	Ig gamma-2b chain
712	81	4.5	585	2	A46507	Ig alpha chain - c	785	79	4.4	659	2	G91009	colicin I receptor
713	81	4.5	588	2	C83836	subtilisin-type pr	786	79	4.4	753	2	G02173	semaphorin III fam
714	81	4.5	637	2	B83052	DnaK protein PA476	787	79	4.4	807	2	A71663	DNA gyrase chain B
715	81	4.5	665	2	E86775	ribonuclease [impo	788	79	4.4	875	2	H90371	proteinase [import
716	80.5	4.5	248	1	Q0B84L	probable glycoprot	789	79	4.4	1175	2	D85089	hypothetical prote
717	80.5	4.5	269	2	B97501	hypothetical prote	790	79	4.4	1204	2	C75015	probable pyrolysin
718	80.5	4.5	273	2	G89856	conserved hypothet	791	79	4.4	1350	2	AF2005	RNA polymerase bet
719	80.5	4.5	277	2	I47162	Ig gamma 4 chain c	792	79	4.4	1439	2	T27110	hypothetical prote
720	80.5	4.5	298	2	T30086	hypothetical prote	793	78.5	4.3	111	2	D37266	Ig kappa chain v r
721	80.5	4.5	327	2	B97076	UDP-glucose 4-epim	794	78.5	4.3	115	2	B46518	Ig I1 chain V regi
722	80.5	4.5	358	2	A99214	suA5 related conse	795	78.5	4.3	140	2	PH1498	Ig heavy chain v r
723	80.5	4.5	459	2	A46254	CD4 precursor - ra	796	78.5	4.3	228	2	S29575	Ig light chain - r
724	80.5	4.5	466	2	AF0616	asparagine-tRNA li	797	78.5	4.3	290	1	XYRBM	arylamine N-acetyl
725	80.5	4.5	517	2	B87646	4-coumarate-CoA li	798	78.5	4.3	323	2	JC2578	DNA repair protein
726	80.5	4.5	554	2	A91250	probable portal pr	799	78.5	4.3	373	2	JH0155	pectin lyase (EC 4
727	80.5	4.5	596	2	D84972	ABC transporter AR	800	78.5	4.3	392	2	T03229	enoyl-lacyl-carrie
728	80.5	4.5	613	2	T41565	hypothetical prote	801	78.5	4.3	434	2	D88305	protein R03D7.4 li
729	80.5	4.5	881	2	S67026	probable membrane	802	78.5	4.3	434	2	S72430	transcription elon
730	80.5	4.5	1025	2	G81722	polymorphic membra	803	78.5	4.3	553	1	SMEBH1	flagellar hook-ass
731	80.5	4.5	1128	1	T08312	plasmid replicatio	804	78.5	4.3	553	2	AM0640	flagellar hook-ass
732	80.5	4.5	1349	2	S51471	killer toxin insen	805	78.5	4.3	556	2	A44441	B-cell antigen CDI
733	80.5	4.5	1375	2	T03345	dextranucrase (EC	806	78.5	4.3	561	2	T45607	hypothetical prote
734	80.5	4.5	1433	2	T30261	chitinase (EC 3.2.	807	78.5	4.3	590	2	A56535	gadd34 protein - l
735	80.5	4.5	1457	1	A48066	protein-tyrosine-p	808	78.5	4.3	592	2	S54489	phosphoribosylamin
736	80.5	4.5	1538	2	E70874	probable ppsB prot	809	78.5	4.3	605	1	A48665	methylmalonyl-CoA
737	80.5	4.5	4588	2	T28667	dynamin beta heavy	810	78.5	4.3	668	2	JQ0773	penicillin-binding
738	80	4.4	104	2	JH0345	T-cell receptor al	811	78.5	4.3	693	2	S46417	heat shock protein
739	80	4.4	150	2	A40862	fibroblast growth	812	78.5	4.3	759	2	B90520	ABC transporter at
740	80	4.4	233	2	I51383	Ig lambda chain -	813	78.5	4.3	783	2	AG3402	polysphosphate kina
741	80	4.4	239	2	G02630	FcalphaRb - human	814	78.5	4.3	829	2	E87305	TonB-dependent rec
742	80	4.4	287	2	JH0332	IgA (Fc) receptor,	815	78.5	4.3	934	2	B29838	parasporal crystal
743	80	4.4	313	2	T28598	hypothetical prote	816	78.5	4.3	1019	2	T40813	probable cell divi
744	80	4.4	425	2	JE0086	SH3-domain binding	817	78.5	4.3	1070	2	T34385	hypothetical prote
745	80	4.4	433	1	S48515	adenylosuccinate s	818	78.5	4.3	1217	2	T00270	hypothetical prote
746	80	4.4	454	1	MHV	Ig mu chain C regi	819	78.5	4.3	1252	2	T31119	msHQ protein - Vib
747	80	4.4	466	2	H96591	secreted protein c	820	78.5	4.3	1385	2	A88554	protein C38C10.5b
748	80	4.4	552	2	S42253	probable N3L prote	821	78.5	4.3	1391	2	B88554	protein-tyrosine-p
749	80	4.4	642	2	S44542	probable membrane	822	78.5	4.3	1440	2	JC6312	vitellogenin II pr
750	80	4.4	680	2	PN0510	integrin beta-3 ch	823	78.5	4.3	1687	2	T43144	probable RTX famil
751	80	4.4	937	2	T04194	hypothetical prote	824	78.5	4.3	5188	2	B85547	hypothetical prote
752	80	4.4	995	2	A56599	embryo kinase 5 -	825	78.5	4.3	5291	2	F90696	hercugulin isoform
753	80	4.4	1200	2	T48194	hypothetical prote	826	78	4.3	125	2	S62676	Ig kappa chain pre
754	80	4.4	3343	2	T42207	breast cancer susc	827	78	4.3	131	2	P01778	Ig light chain v r
755	79.5	4.4	155	2	A41675	telokin - rabbit	828	78	4.3	132	2	AS5410	Ig kappa chain v r
756	79.5	4.4	204	2	A69197	hypothetical prote	829	78	4.3	137	2	C45893	T-cell receptor al
757	79.5	4.4	220	2	I55963	Lyt-2.1 lymphocyte	830	78	4.3	178	2	G71195	hypothetical prote
758	79.5	4.4	250	2	A34342	IgE Fc receptor al	831	78	4.3	233	2	S29577	Ig light chain - r
759	79.5	4.4	261	2	S29360	Fc gamma (15G) rec	832	78	4.3	255	2	JC7593	SH2 domain-contain

833	78	4.3	301	1	G64491	thioredoxin-dsulf	906	76.5	4.2	267	1	RWMS8	T-cell receptor al
834	78	4.3	328	1	I47158	Ig gamma 1 chain c	907	76.5	4.2	299	1	AHRB	Ig alpha chain C r
835	78	4.3	370	1	HLHUA3	MHC class I histoc	908	76.5	4.2	306	2	B75129	thiamin biosynthes
836	78	4.3	413	2	AG3267	amino-acid N-acety	909	76.5	4.2	332	2	D83745	3-oxacyl-lacyl-ca
837	78	4.3	460	2	S67174	hypothetical prote	910	76.5	4.2	403	2	S53477	IMP dehydrogenase
838	78	4.3	475	2	T44566	conserved hypotet	911	76.5	4.2	428	2	AH3536	dihyroliposamide S
839	78	4.3	481	2	B82217	asparaginyl-tRNA s	912	76.5	4.2	431	2	A86601	hypothetical prote
840	78	4.3	542	2	A84554	hypothetical prote	913	76.5	4.2	431	2	G72022	probable sodium-tr
841	78	4.3	702	2	T21148	hypothetical prote	914	76.5	4.2	457	2	A27449	T-cell surface gly
842	78	4.3	874	2	C84513	Mutator-like trans	915	76.5	4.2	463	2	T14884	hypothetical prote
843	78	4.3	980	2	H90881	probable flagellin	916	76.5	4.2	483	2	A69745	hypothetical prote
844	78	4.3	980	2	D85532	probable structura	917	76.5	4.2	515	2	H86202	hypothetical prote
845	78	4.3	1016	2	H71460	probable outer mem	918	76.5	4.2	516	2	E70035	levanase homolog y
846	78	4.3	1029	2	F96602	hypothetical prote	919	76.5	4.2	528	2	PC4025	intercellular adhe
847	78	4.3	1138	1	S24066	protein-tyrosine k	920	76.5	4.2	547	2	S75904	hypothetical prote
848	78	4.3	1217	2	F97177	alpha-glucosidase	921	76.5	4.2	563	2	T20631	hypothetical prote
849	78	4.3	2185	1	GNYSV	genome polyprotein	922	76.5	4.2	572	1	HNN2B3	hemagglutinin-neur
850	78	4.3	2256	2	AD1018	large repetitive p	923	76.5	4.2	573	2	F99719	protein F99812.1 l
851	78	4.3	4302	2	A38971	polycystic kidney	924	76.5	4.2	573	2	T20632	hypothetical prote
852	77.5	4.3	119	2	PH1519	Ig heavy chain V r	925	76.5	4.2	622	2	A36915	fructanase - Bacte
853	77.5	4.3	140	2	A36194	Ig heavy chain V r	926	76.5	4.2	653	2	B90908	probable host spec
854	77.5	4.3	284	2	S75817	hypothetical prote	927	76.5	4.2	656	2	B71290	conserved hypotet
855	77.5	4.3	307	2	C71002	hypothetical prote	928	76.5	4.2	740	2	AD0485	probable exported
856	77.5	4.3	309	2	T15747	hypothetical prote	929	76.5	4.2	749	2	E86774	hypothetical prote
857	77.5	4.3	315	1	HNV2VT	hemagglutinin prec	930	76.5	4.2	775	2	G90996	probable host spec
858	77.5	4.3	428	2	T48167	hypothetical prote	931	76.5	4.2	782	2	A85693	hypothetical prote
859	77.5	4.3	446	2	S40295	Ig gamma-2a chain	932	76.5	4.2	896	2	T22061	hypothetical prote
860	77.5	4.3	466	2	C85619	asparagine tRNA sy	933	76.5	4.2	913	2	E75554	valyl-tRNA synthet
861	77.5	4.3	466	2	E90755	asparagine tRNA sy	934	76.5	4.2	1039	2	T30856	protein F2 - Strep
862	77.5	4.3	469	1	TVHUE2	transcription fact	935	76.5	4.2	1124	1	I58388	protein-tyrosine k
863	77.5	4.3	532	2	C42804	immunodominant typ	936	76.5	4.2	1131	2	T14517	hypothetical prote
864	77.5	4.3	534	2	S62005	phosphonoacetaldeh	937	76.5	4.2	1151	2	S48431	probable membrane
865	77.5	4.3	584	2	F70522	probable polyketid	938	76.5	4.2	1248	2	C89874	autolysin [impor
866	77.5	4.3	593	2	A11235	internalin protein	939	76.5	4.2	1363	2	C84346	hypothetical prote
867	77.5	4.3	655	2	T34219	hypothetical prote	940	76.5	4.2	1377	2	I54632	hypothetical prote
868	77.5	4.3	668	2	S49639	probable membrane	941	76.5	4.2	1648	2	S61654	probable membrane
869	77.5	4.3	676	2	T30480	envelope protein h	942	76.5	4.2	2477	2	S14428	fibronectin precur
870	77.5	4.3	852	1	VCLJGG	env polyprotein pr	943	76	4.2	91	2	PH1071	Ig light chain V r
871	77.5	4.3	888	2	A54280	cell differentiat	944	76	4.2	107	2	PD0011	Ig kappa chain V r
872	77.5	4.3	1192	2	T08609	hypothetical prote	945	76	4.2	108	2	G30560	Ig kappa chain V r
873	77.5	4.3	1474	2	F69009	probable membrane	946	76	4.2	108	2	S38720	Ig kappa chain V r
874	77.5	4.3	1515	2	A40203	4-alpha-glucanotra	947	76	4.2	118	2	I33932	Ig light chain pre
875	77.5	4.3	1819	2	D97033	uncharacterized pr	948	76	4.2	120	2	C29775	Ig kappa chain pre
876	77.5	4.3	1825	2	C88400	protein H19M22.1 l	949	76	4.2	161	2	S04931	T-cell receptor de
877	77.5	4.3	1825	2	T32828	hypothetical prote	950	76	4.2	251	2	S64927	probable membrane
878	77.5	4.3	3329	2	T42205	breast cancer susc	951	76	4.2	254	2	B75052	coenzyme pqq synth
879	77.5	4.3	3329	2	T30904	breast cancer tumo	952	76	4.2	310	2	F90011	conserved hypotet
880	77.5	4.3	3591	1	S21010	filamentous hemagg	953	76	4.2	327	2	T07104	2'-hydroxydihydrod
881	77	4.3	107	2	PC4405	Ig kappa chain V r	954	76	4.2	327	2	S06611	Ig gamma-2 chain C
882	77	4.3	128	2	S40343	Ig kappa chain V r	955	76	4.2	365	2	D87526	hypothetical prote
883	77	4.3	234	2	S01320	Ig kappa chain pre	956	76	4.2	426	2	H84846	probable polygalac
884	77	4.3	302	2	S05079	hypothetical prote	957	76	4.2	430	2	T28143	tapsain 1 homolog,
885	77	4.3	328	2	I47161	Ig gamma 3 chain C	958	76	4.2	431	2	F71476	probable sodium-tr
886	77	4.3	338	2	S09276	Ig alpha chain C r	959	76	4.2	450	1	MHDG	Ig mu chain C regi
887	77	4.3	384	2	E84871	probable polygalac	960	76	4.2	473	2	H83676	pyruvate dehydroge
888	77	4.3	439	2	AE1251	probable peptidogl	961	76	4.2	501	2	E96509	protein P27F5.17 l
889	77	4.3	614	2	A88466	protein B0244.2 l	962	76	4.2	506	1	ACRYG1	nicotinic acetylch
890	77	4.3	817	2	F86742	ribonuclease [impo	963	76	4.2	511	2	E84685	probable seed stor
891	77	4.3	859	2	AC2089	adenylate cyclase	964	76	4.2	516	2	A44494	CAMP-responsive el
892	77	4.3	879	2	C90879	hypothetical prote	965	76	4.2	577	2	T48530	clathrin binding p
893	77	4.3	879	2	G85739	hypothetical prote	966	76	4.2	656	2	AC0429	2',3'-cyclic-nucle
894	77	4.3	928	2	A87749	protein F55C7.7c l	967	76	4.2	859	1	VCLJCT	env polyprotein pr
895	77	4.3	976	2	C96958	ACT domain contain	968	76	4.2	1020	2	A46405	C protein alpha an
896	77	4.3	1071	1	PXBVYA	H+-exporting ATPas	969	76	4.2	1151	2	S03722	DNA-directed DNA p
897	77	4.3	1176	2	A33856	surface-layer 125K	970	76	4.2	1196	2	H86389	hypothetical prote
898	77	4.3	2488	2	T42739	guanine nucleotide	971	76	4.2	1278	2	A47462	probable DNA-direc
899	77	4.3	3562	2	A47171	chondroitin sulfat	972	76	4.2	1366	2	S57664	IgA-specific metal
900	76.5	4.2	135	2	PH1492	Ig heavy chain V r	973	76	4.2	2380	2	T29551	hypothetical prote
901	76.5	4.2	136	2	A49137	Ig kappa chain pre	974	75.5	4.2	104	2	JC6076	anti-D-dimer monoc
902	76.5	4.2	178	2	S29594	Ig gamma chain (WM	975	75.5	4.2	114	2	S44119	Ig kappa chain V-J
903	76.5	4.2	232	2	S17399	Ig lambda chain (WM	976	75.5	4.2	123	2	S35479	Ig kappa chain pre
904	76.5	4.2	236	2	A24637	T-cell surface gly	977	75.5	4.2	131	2	S09259	Ig kappa chain pre
905	76.5	4.2	252	2	AF2719	arginine-tRNA-prot	978	75.5	4.2	131	2	D29380	Ig kappa chain pre

979	75.5	4.2	132	2	PH0106	anti-digoxin trans	1052	75	4.2	1311	2	T33757	hypothetical prote
980	75.5	4.2	133	2	S40324	Ig kappa chain V r	1053	75	4.2	1313	2	G82887	hypothetical prote
981	75.5	4.2	140	1	HVMSG7	Ig heavy chain pre	1054	75	4.2	1476	2	A22220	hypothetical prote
982	75.5	4.2	140	1	PH1489	Ig heavy chain V r	1055	75	4.2	1661	2	H71439	hypothetical prote
983	75.5	4.2	189	2	T39849	anaphase promoting	1056	75	4.2	1672	2	T46237	hypothetical prote
984	75.5	4.2	231	2	PC4155	Ig gamma-2b chain	1057	75	4.2	2291	2	S11238	polymerase - Berne
985	75.5	4.2	234	2	A39956	Ig lambda chain pr	1058	75	4.2	2413	2	S34670	splicing factor PR
986	75.5	4.2	248	2	F96655	hypothetical prote	1059	75	4.2	2500	2	G71609	hypothetical prote
987	75.5	4.2	249	2	C69081	acetyl-CoA synthet	1060	74.5	4.1	116	1	HVMS1B	Ig heavy chain pre
988	75.5	4.2	262	2	T42986	v-cyclin - ateline	1061	74.5	4.1	119	2	PH1517	Ig heavy chain V r
989	75.5	4.2	316	2	F86157	hypothetical prote	1062	74.5	4.1	119	2	PH1516	Ig heavy chain V r
990	75.5	4.2	341	2	S72445	DNA-binding protei	1063	74.5	4.1	140	2	PH1488	Ig heavy chain V r
991	75.5	4.2	362	2	S16303	polygalacturonase	1064	74.5	4.1	192	2	T02893	hypothetical prote
992	75.5	4.2	398	2	T46475	hypothetical prote	1065	74.5	4.1	232	2	S25756	Ig lambda chain -
993	75.5	4.2	402	2	F70850	DNA-directed DNA p	1066	74.5	4.1	243	2	AC3071	transcription regu
994	75.5	4.2	504	2	S00390	Ig gamma chain (cl	1067	74.5	4.1	277	2	S29922	Salu8L protein pre
995	75.5	4.2	524	2	D87440	2-isopropylmalate	1068	74.5	4.1	370	1	HVRKCS	Ig mu chain C regi
996	75.5	4.2	569	2	A46462	T cell activation	1069	74.5	4.1	397	2	S70987	dnaN protein - Myc
997	75.5	4.2	580	2	S49308	beta-fructofuranos	1070	74.5	4.1	438	2	B97712	hypothetical prote
998	75.5	4.2	582	2	S53814	DEAD box protein -	1071	74.5	4.1	466	1	SYECNT	asparagine-tRNA li
999	75.5	4.2	641	2	JC7142	dextranase (EC 3.2	1072	74.5	4.1	468	1	P2WL51	L2 protein - human
1000	75.5	4.2	691	1	S46735	NADPH-ferrihemopro	1073	74.5	4.1	501	2	S74341	hypothetical prote
1001	75.5	4.2	710	1	A46273	mitochondrial inte	1074	74.5	4.1	549	2	S04845	Ig heavy chain pre
1002	75.5	4.2	713	1	ALBSG7	cyclomaltodextrin	1075	74.5	4.1	591	1	CBY2	L-lactate dehydrog
1003	75.5	4.2	739	2	A55314	glycine-tRNA ligas	1076	74.5	4.1	644	2	S50552	hypothetical prote
1004	75.5	4.2	746	2	E64701	conserved hypothet	1077	74.5	4.1	663	2	AG0782	colicin I receptor
1005	75.5	4.2	771	2	B70564	hypothetical prote	1078	74.5	4.1	693	2	JN0843	heat shock protein
1006	75.5	4.2	815	2	AB2444	hypothetical prote	1079	74.5	4.1	729	2	T46270	hypothetical prote
1007	75.5	4.2	857	1	S05943	gelation factor -	1080	74.5	4.1	807	2	T39479	histone transcript
1008	75.5	4.2	918	2	D71407	hypothetical prote	1081	74.5	4.1	862	2	E88594	protein Y48A6B.11
1009	75.5	4.2	1068	2	S73091	hypothetical prote	1082	74.5	4.1	899	2	A83019	conserved hypothet
1010	75.5	4.2	1787	2	A99273	hypothetical prote	1083	74.5	4.1	947	2	T26314	hypothetical prote
1011	75.5	4.2	1818	2	AE3011	conserved hypothet	1084	74.5	4.1	1043	2	D84900	hypothetical prote
1012	75.5	4.2	1871	2	D96698	probable DNA polym	1085	74.5	4.1	1183	2	S63046	probable membrane
1013	75.5	4.2	1894	2	T02155	DNA-directed DNA p	1086	74.5	4.1	1403	2	T11583	probable translati
1014	75.5	4.2	2265	1	FNBO	fibronectin - bovi	1087	74.5	4.1	1622	2	T45240	hypothetical prote
1015	75.5	4.2	5005	2	F82884	hypothetical prote	1088	74.5	4.1	1825	2	S13507	microtubule-associ
1016	75.5	4.2	6669	2	S55024	nebulin, skeletal	1089	74.5	4.1	1830	2	A37981	microtubule-associ
1017	75	4.2	106	2	A49138	IgA kappa rheumato	1090	74.5	4.1	2338	2	T73957	kinase-related pro
1018	75	4.2	115	2	B26524	T-cell receptor be	1091	74.5	4.1	2366	2	S10317	toxin B - Clostrid
1019	75	4.2	117	2	S40362	Ig kappa chain - h	1092	74.5	4.1	2761	2	T21064	hypothetical prote
1020	75	4.2	128	2	A47159	Ig lambda chain V	1093	74.5	4.1	4572	2	S57908	hypothetical 527K
1021	75	4.2	130	2	C29380	Ig kappa chain pre	1094	74.5	4.1	4639	1	A54794	dysin heavy chain
1022	75	4.2	131	2	D34904	Ig kappa chain pre	1095	74	4.1	107	2	S12954	Ig kappa chain V r
1023	75	4.2	148	2	PH0115	Ig heavy chain pre	1096	74	4.1	108	2	T26681	hypothetical prote
1024	75	4.2	157	2	D31327	IgE receptor alpha	1097	74	4.1	131	2	S52449	Ig kappa chain V r
1025	75	4.2	215	2	A57843	sodium channel bet	1098	74	4.1	196	2	S72716	4-coumarate-CoA li
1026	75	4.2	246	2	E69230	hypothetical prote	1099	74	4.1	221	1	Q0BE48	BART1 protein - hu
1027	75	4.2	268	2	A56446	Ig heavy chain V r	1100	74	4.1	231	2	S25751	Ig lambda chain -
1028	75	4.2	283	2	AH1767	protoporphyrinogen	1101	74	4.1	248	2	B45831	MHC class I histoc
1029	75	4.2	285	2	B82842	spermidine synthas	1102	74	4.1	277	2	D42521	A38L protein - vac
1030	75	4.2	297	2	AC2380	hypothetical prote	1103	74	4.1	365	2	I37476	MHC class I histoc
1031	75	4.2	307	1	RWMSBC	T-cell receptor be	1104	74	4.1	365	2	I56039	HLA-A30.3 precurs
1032	75	4.2	321	2	S10006	hypothetical prote	1105	74	4.1	365	2	I38519	MHC class I histoc
1033	75	4.2	359	2	AF3184	beta-lactanase [im	1106	74	4.1	416	1	A41267	transcription fact
1034	75	4.2	364	2	S03535	class I histocompa	1107	74	4.1	429	2	AC1522	flagellar hook-ass
1035	75	4.2	392	2	T34095	zinc finger protei	1108	74	4.1	438	1	HVRKCS	Ig mu chain C regi
1036	75	4.2	393	2	T03216	enoyl-l-acyl-carrie	1109	74	4.1	449	1	B64706	hemolysin - Helic
1037	75	4.2	394	2	G69230	endo-1,4-beta-gluc	1110	74	4.1	454	2	T26296	hypothetical prote
1038	75	4.2	416	2	E64140	hypothetical prote	1111	74	4.1	461	1	HVRKCO	Ig mu chain C regi
1039	75	4.2	435	2	T42613	probable envelope	1112	74	4.1	468	1	TVMSE2	transcription fact
1040	75	4.2	439	2	G97159	contains cell adhe	1113	74	4.1	474	2	T47299	hypothetical prote
1041	75	4.2	444	2	B90053	hypothetical prote	1114	74	4.1	514	2	G89903	conserved hypothet
1042	75	4.2	476	2	S64291	hypothetical prote	1115	74	4.1	523	2	F85489	2-isopropylmalate
1043	75	4.2	479	1	VGBEF2	glycoprotein F - h	1116	74	4.1	523	2	F90638	2-isopropylmalate
1044	75	4.2	535	2	S76564	hypothetical prote	1117	74	4.1	523	2	B64729	hypothetical prote
1045	75	4.2	574	2	T29005	hypothetical prote	1118	74	4.1	562	2	AH2084	laccase (EC 1.10.3
1046	75	4.2	577	2	IS0731	Ig heavy chain - n	1119	74	4.1	573	2	T02743	probable acyl-CoA
1047	75	4.2	701	2	C97910	ATP-dependent prot	1120	74	4.1	579	2	D87063	hypothetical prote
1048	75	4.2	743	2	T34853	probable fusidic a	1121	74	4.1	581	2	S63033	hypothetical prote
1049	75	4.2	775	1	JQ1639	outer layer protei	1122	74	4.1	707	2	C97302	subtilisin-like pr
1050	75	4.2	780	2	T31548	hypothetical prote	1123	74	4.1	755	2	T48553	WD40-repeat protei
1051	75	4.2	1242	1	DJBEC1	DNA-directed DNA p	1124	74	4.1	876	2	T51507	

1125	74	4.1	879	2	H64888	membrane protein y	1198	73	4.0	469	2	D95989	conserved hypochet
1126	74	4.1	908	2	T25035	hypothetical prote	1199	73	4.0	478	2	S47040	gene Tt52 protein
1127	74	4.1	966	2	E87473	TonB-dependent rec	1200	73	4.0	481	2	C97238	Arg dependent RNA
1128	74	4.1	1085	2	JC2227	probable helicase	1201	73	4.0	523	2	A12696	serine proteinase
1129	74	4.1	1128	2	H90538	hypothetical prote	1202	73	4.0	523	2	A97479	probable serine pr
1130	74	4.1	1132	1	QSBFL	host specificity p	1203	73	4.0	565	2	H69342	GTP-binding protei
1131	74	4.1	1136	1	S57845	protein-tyrosine k	1204	73	4.0	586	2	T45945	laccase-like prote
1132	74	4.1	1137	2	B90734	probable host spec	1205	73	4.0	657	2	AD1525	probable cell surf
1133	74	4.1	1482	2	S13495	pregnancy zone pro	1206	73	4.0	671	2	T23015	hypothetical prote
1134	74	4.1	1488	2	C70984	probable p8E prot	1207	73	4.0	673	2	H86761	glycine-tRNA ligase
1135	74	4.1	1524	2	A96950	DNA segregation AT	1208	73	4.0	673	2	T41768	AcMNPV orf23 - Bom
1136	74	4.1	1963	2	B98002	IgA-specific metal	1209	73	4.0	688	2	S39491	proteochlorophyllid
1137	74	4.1	2185	1	GNNYSH	genome polyprotein	1210	73	4.0	701	2	H95039	hypothetical prote
1138	74	4.1	2812	2	T43271	phosphatidylinosit	1211	73	4.0	722	2	D70200	polyribonucleotide
1139	73.5	4.1	64	2	S20961	keratinocyte growt	1212	73	4.0	745	2	B33856	hypothetical 80K p
1140	73.5	4.1	96	2	PH1070	Ig light chain v r	1213	73	4.0	754	2	E86592	general secretion
1141	73.5	4.1	97	2	S26341	Ig light chain v r	1214	73	4.0	754	2	D72032	general secretion
1142	73.5	4.1	119	2	PH1510	Ig heavy chain v r	1215	73	4.0	771	2	AF2056	cation transportin
1143	73.5	4.1	119	2	PH1518	Ig heavy chain v r	1216	73	4.0	772	2	A46108	outer capsid prote
1144	73.5	4.1	133	2	PC1155	Ig heavy chain pre	1217	73	4.0	858	2	T12142	lipoxigenase (EC 1
1145	73.5	4.1	133	2	PH1493	Ig heavy chain v r	1218	73	4.0	870	2	T47454	lipoxigenase AtLOX
1146	73.5	4.1	135	2	PH1486	Ig heavy chain v r	1219	73	4.0	896	2	JQ2391	lipoxigenase (EC 1
1147	73.5	4.1	140	2	PH1483	Ig heavy chain v r	1220	73	4.0	897	2	S67283	hypothetical prote
1148	73.5	4.1	229	2	A20969	Ig kappa chain pre	1221	73	4.0	935	2	S66306	hypothetical prote
1149	73.5	4.1	309	2	T09564	glutamyl-peptide	1222	73	4.0	980	2	T39630	valine-tRNA ligase
1150	73.5	4.1	339	2	T28138	Ig V-region-like B	1223	73	4.0	1095	2	T24061	hypothetical prote
1151	73.5	4.1	340	2	T28137	Ig V-region-like B	1224	73	4.0	1336	2	T18288	ABC transport prote
1152	73.5	4.1	366	2	AF0497	DNA-directed DNA p	1225	73	4.0	1473	2	A35186	salivary agglutini
1153	73.5	4.1	380	2	S12839	Ig heavy chain pre	1226	73	4.0	1518	2	T28880	hypothetical prote
1154	73.5	4.1	388	2	E95007	sugar isomerase do	1227	73	4.0	1815	2	B95942	conserved hypochet
1155	73.5	4.1	400	2	T22853	probable cathepsin	1228	73	4.0	2207	2	S09553	genome polyprotein
1156	73.5	4.1	418	2	G87469	ThiG/Pfpi family p	1229	73	4.0	2210	1	RRXPTV	genome polyprotein
1157	73.5	4.1	422	2	A96912	glutamate-1-semial	1230	73	4.0	2907	2	A57278	fibrillin-2 precur
1158	73.5	4.1	431	2	S37775	filamin, muscle -	1231	73	4.0	3011	1	S40770	genome polyprotein
1159	73.5	4.1	505	2	AC3486	cell surface prote	1232	73	4.0	3263	2	E82410	hypothetical prote
1160	73.5	4.1	579	2	B84956	cell division prot	1233	73	4.0	4688	2	F82885	hypothetical prote
1161	73.5	4.1	632	2	C98264	5'-nucleotidase pr	1234	73	4.0	4936	2	AH2515	hypothetical prote
1162	73.5	4.1	636	2	AF3020	5'-nucleotidase [i	1235	72.5	4.0	124	2	S40364	Ig kappa chain - h
1163	73.5	4.1	677	2	T40145	probable beta-adap	1236	72.5	4.0	126	2	S40312	Ig kappa chain - h
1164	73.5	4.1	725	2	C87485	ComEC/Rec2 family	1237	72.5	4.0	128	2	S20636	Ig heavy chain var
1165	73.5	4.1	815	2	E70021	3-hydroxyacyl-CoA	1238	72.5	4.0	137	2	E34903	Ig heavy chain var
1166	73.5	4.1	941	2	S29043	cellulase (EC 3.2.	1239	72.5	4.0	141	2	T19797	Ig heavy chain var
1167	73.5	4.1	986	2	B81675	polymorphic membra	1240	72.5	4.0	198	2	G75153	hypothetical prote
1168	73.5	4.1	1005	2	T18537	Ig heavy chain - c	1241	72.5	4.0	199	2	G75153	hypothetical prote
1169	73.5	4.1	1052	2	H83309	cell wall-associat	1242	72.5	4.0	215	2	I64004	hypothetical prote
1170	73.5	4.1	1119	2	A86340	protein F2D10.24 [1243	72.5	4.0	219	2	S38865	Ig kappa chain - m
1171	73.5	4.1	1121	2	T38127	phosphoprotein pho	1244	72.5	4.0	233	1	JU0284	Fe gamma (IgG) rec
1172	73.5	4.1	1280	2	T00365	hypothetical prote	1245	72.5	4.0	247	2	PQ0655	outer capsid spike
1173	73.5	4.1	1285	2	B72420	hypothetical prote	1246	72.5	4.0	247	2	PQ0655	outer capsid spike
1174	73.5	4.1	1292	2	T09229	galactose binding	1247	72.5	4.0	247	2	PQ0657	T-cell receptor al
1175	73.5	4.1	1330	1	QQFEB	epidermal growth f	1248	72.5	4.0	264	2	F27579	T-cell receptor be
1176	73.5	4.1	1487	2	S15904	alpha-1 proteinase	1249	72.5	4.0	267	2	PL0064	hypothetical prote
1177	73.5	4.1	1571	2	T00062	hypothetical prote	1250	72.5	4.0	286	2	S32480	Ig heavy chain VDJ
1178	73.5	4.1	3328	2	T30835	breast cancer tumo	1251	72.5	4.0	288	2	S29690	B7 protein - red-c
1179	73	4.0	126	2	S24704	Ig heavy chain V6	1252	72.5	4.0	289	2	G00031	adenine-specific m
1180	73	4.0	127	2	PH1224	Ig kappa chain pre	1253	72.5	4.0	312	2	D82690	hypothetical prote
1181	73	4.0	128	2	FN0445	Ig kappa chain pre	1254	72.5	4.0	322	2	T50167	hypothetical prote
1182	73	4.0	131	2	E25733	T-cell receptor al	1255	72.5	4.0	350	2	T21106	hypothetical prote
1183	73	4.0	132	2	A27632	Ig kappa chain pre	1256	72.5	4.0	377	2	T05453	trehalose-6-phosph
1184	73	4.0	133	1	K4HJUI	T-cell receptor al	1257	72.5	4.0	401	2	E87531	hypothetical prote
1185	73	4.0	145	2	S21651	T-cell receptor be	1258	72.5	4.0	408	2	D95417	probable ABC trans
1186	73	4.0	225	2	E82473	hypothetical prote	1259	72.5	4.0	423	2	F64436	hypothetical prote
1187	73	4.0	233	2	S25747	Ig lambda chain -	1260	72.5	4.0	423	2	B84964	adenosylmethionine
1188	73	4.0	332	2	G83458	sulfate-binding pr	1261	72.5	4.0	431	2	T48340	hypothetical prote
1189	73	4.0	339	2	T08782	hypothetical prote	1262	72.5	4.0	453	2	C31933	Ig mu chain C regi
1190	73	4.0	389	2	B42708	serine-type D-Ala-	1263	72.5	4.0	475	2	S01321	Ig gamma-2b chain
1191	73	4.0	393	1	HVRK1	Ig mu chain C regi	1264	72.5	4.0	482	2	T49079	serine-type carbox
1192	73	4.0	438	1	HVRK2	Ig mu chain C regi	1265	72.5	4.0	498	2	G97279	protein containing
1193	73	4.0	445	2	S67695	26S proteasome reg	1266	72.5	4.0	503	2	B72289	oligopeptide ABC t
1194	73	4.0	451	1	S75239	hypothetical prote	1267	72.5	4.0	527	2	T22000	hypothetical prote
1195	73	4.0	454	2	AE1970	hypothetical prote	1268	72.5	4.0	533	2	A42349	aspartic proteinas
1196	73	4.0	469	1	P2WL35	L2 protein - human	1269	72.5	4.0	560	2	B81451	flagellar M-ring p
1197	73	4.0	469	2	S36525	L2 protein - human	1270	72.5	4.0	668	2	T05803	hypothetical prote

1271	72.5	4.0	676	2	F69276	conserved hypothet	1344	72	4.0	992	2	T46337	hypothetical prote
1272	72.5	4.0	736	2	D96830	probable heat-shoc	1345	72	4.0	1076	1	A35622	nuclear pore prote
1273	72.5	4.0	759	1	B60008	RNA-directed RNA p	1346	72	4.0	1083	2	S48460	probable membrane
1274	72.5	4.0	836	2	A69550	hypothetical prote	1347	72	4.0	1106	2	A97647	cation efflux syst
1275	72.5	4.0	887	1	IJCHCL	E-cadherin precurs	1348	72	4.0	1106	2	A92870	Acr family transpo
1276	72.5	4.0	894	2	S61015	hypothetical prote	1349	72	4.0	1132	2	H90834	host specificity p
1277	72.5	4.0	941	2	F97353	uncharacterized co	1350	72	4.0	1149	2	T27567	hypothetical prote
1278	72.5	4.0	954	2	S57108	hypothetical prote	1351	72	4.0	1155	2	H71456	probable prolysin
1279	72.5	4.0	970	2	I78842	receptor protein-t	1352	72	4.0	1199	2	S77082	pyruvate [laxodox
1280	72.5	4.0	1039	2	T15885	hypothetical prote	1353	72	4.0	1245	1	VHWB2	structural polypro
1281	72.5	4.0	1166	2	T29009	hypothetical prote	1354	72	4.0	1391	2	S50608	hypothetical prote
1282	72.5	4.0	1186	2	T42729	histocompatibility	1355	72	4.0	1408	2	H69068	cell surface glyco
1283	72.5	4.0	1212	2	T42387	histocompatibility	1356	72	4.0	2094	2	S33124	tptr protein - huma
1284	72.5	4.0	1228	2	G90581	hypothetical prote	1357	72	4.0	2567	2	A49551	filamin, Muller ce
1285	72.5	4.0	1229	2	T25697	hypothetical prote	1358	72	4.0	2902	2	C71953	coxin-like outer m
1286	72.5	4.0	1276	2	B86546	polymorphic prote	1359	72	4.0	3890	2	C89921	hypothetical prote
1287	72.5	4.0	1276	2	C81591	polymorphic membra	1360	72	4.0	8563	2	T30226	polyketide synthas
1288	72.5	4.0	1306	2	S22624	aggregation protei	1361	71.5	4.0	91	2	S17628	IG kappa chain V r
1289	72.5	4.0	1383	2	T11052	guanine nucleotide	1362	71.5	4.0	119	2	PH1503	IG heavy chain V r
1290	72.5	4.0	1431	2	A45866	dextranucrase (EC	1363	71.5	4.0	121	2	S44113	IG heavy chain V r
1291	72.5	4.0	1500	1	JQ1348	carbamoyl-phosphat	1364	71.5	4.0	129	2	S40347	IG kappa chain - h
1292	72.5	4.0	1665	2	T29008	hypothetical prote	1365	71.5	4.0	225	2	JL0029	IG kappa chain - h
1293	72.5	4.0	1966	2	T08991	hypothetical prote	1366	71.5	4.0	246	1	A32999	myelin P0 protein
1294	72.5	4.0	2004	2	F95133	immunoglobulin A1	1367	71.5	4.0	275	2	H35216	FP31 protein - fow
1295	72.5	4.0	2052	2	C97038	phage-related prot	1368	71.5	4.0	275	2	C82752	hypothetical prote
1296	72.5	4.0	324	2	S37431	ankyrin 2, neurona	1369	71.5	4.0	290	2	T40852	cystathionine beta
1297	72.5	4.0	4845	2	T31067	BIR repeat contain	1370	71.5	4.0	303	2	H71693	hypothetical prote
1298	72	4.0	115	1	KVM5K2	IG kappa chain pre	1371	71.5	4.0	305	2	B84413	hypothetical prote
1299	72	4.0	115	2	A30995	T-cell receptor be	1372	71.5	4.0	321	2	F71163	probable oligopept
1300	72	4.0	131	2	B34904	IG kappa chain pre	1373	71.5	4.0	325	2	H90269	hypothetical prote
1301	72	4.0	131	2	B30577	IG kappa chain pre	1374	71.5	4.0	326	1	G2HU	IG gamma-2 chain C
1302	72	4.0	133	2	I45927	membrane-bound imm	1375	71.5	4.0	340	2	S20879	homotetic protein H
1303	72	4.0	148	2	PH0121	IG heavy chain pre	1376	71.5	4.0	360	2	H95980	probable uroporphyr
1304	72	4.0	148	2	PH0119	IG heavy chain pre	1377	71.5	4.0	361	2	S78542	drdGlucose 4,6-de
1305	72	4.0	208	1	WMNV15	18-5K protein - Au	1378	71.5	4.0	384	2	AI2962	cellulose synthesi
1306	72	4.0	223	2	I46696	CTLA-4 precursor -	1379	71.5	4.0	389	2	E98320	hypothetical prote
1307	72	4.0	239	2	F81795	probable periplasm	1380	71.5	4.0	476	2	A46118	myosin-binding pro
1308	72	4.0	338	2	A53066	CCAR enhancer-bin	1381	71.5	4.0	477	2	JC4386	adenyl cyclase-a
1309	72	4.0	340	2	T02639	Gs protein homolog	1382	71.5	4.0	493	2	S32999	hexon protein - hu
1310	72	4.0	349	2	F70357	lipoprotein - Aquil	1383	71.5	4.0	507	1	A43387	polymerase-associ
1311	72	4.0	351	2	JQ2166	spindle body prote	1384	71.5	4.0	507	2	AC3036	glycerol-3-phospha
1312	72	4.0	372	1	UHUCN	ciliary neurotroph	1385	71.5	4.0	507	2	H98249	glpD gene homolog
1313	72	4.0	375	2	A64398	hypothetical prote	1386	71.5	4.0	520	2	AI3295	adenylouccinate s
1314	72	4.0	386	2	B84562	probable Tub famil	1387	71.5	4.0	523	1	S48997	IMP dehydrogenase
1315	72	4.0	411	1	VBEG2	Glycoprotein G pre	1388	71.5	4.0	572	2	B46529	IG Y heavy chain (
1316	72	4.0	424	2	A37755	xyylanase (EC 3.2.1	1389	71.5	4.0	592	2	JC4642	purH bifunctional
1317	72	4.0	424	2	H96963	dihydroorotase [im	1390	71.5	4.0	608	2	T32708	hypothetical prote
1318	72	4.0	425	2	AC2959	HlyD family secret	1391	71.5	4.0	611	2	T45493	glutamine-fructose
1319	72	4.0	428	2	T08626	sarcosine reductas	1392	71.5	4.0	647	2	F70057	penicillin-binding
1320	72	4.0	430	2	T32055	hypothetical prote	1393	71.5	4.0	659	2	S38551	El protein - human
1321	72	4.0	433	2	S76485	hypothetical prote	1394	71.5	4.0	668	2	T44118	penicillin-binding
1322	72	4.0	441	2	AF0048	modification methy	1395	71.5	4.0	668	2	JQ0774	penicillin-binding
1323	72	4.0	452	2	C98324	hypothetical prote	1396	71.5	4.0	751	2	AI3392	phosphoribosylform
1324	72	4.0	454	2	A46532	IG mu chain C regi	1397	71.5	4.0	775	1	I37422	glutamine-tRNA lig
1325	72	4.0	513	2	D96943	Probable polygalac	1398	71.5	4.0	775	2	S32494	transposable eleme
1326	72	4.0	515	2	AH2996	glycerol-3-phospha	1399	71.5	4.0	776	2	S53790	hypothetical prote
1327	72	4.0	531	2	A98287	glpD gene homolog	1400	71.5	4.0	860	2	ACU582	leucyl-CRNA synth
1328	72	4.0	531	2	T50964	related to RCC1 pr	1401	71.5	4.0	893	2	F86476	protein F1504.39 (
1329	72	4.0	570	2	A57535	interleukin 1 recep	1402	71.5	4.0	928	2	C97728	hypothetical prote
1330	72	4.0	570	2	T64414	hypothetical prote	1403	71.5	4.0	958	2	S32435	Na+/Ca2+-exchangin
1331	72	4.0	574	2	E64414	hypothetical prote	1404	71.5	4.0	1021	2	T15765	hypothetical prote
1332	72	4.0	576	2	G81657	DNA mismatch repai	1405	71.5	4.0	1025	2	T10259	RNA-directed DNA p
1333	72	4.0	627	2	S14683	IG mu chain precur	1406	71.5	4.0	1031	2	D88912	hypothetical prote
1334	72	4.0	665	2	F97032	beta-glucosidase f	1407	71.5	4.0	1031	2	T33655	hypothetical prote
1335	72	4.0	697	2	T27587	hypothetical prote	1408	71.5	4.0	1094	2	S22573	DNAB-dependent rec
1336	72	4.0	777	1	TVVPCP	large T antigen -	1409	71.5	4.0	1125	2	H87644	plasmid replicatio
1337	72	4.0	782	2	S22560	large T antigen -	1410	71.5	4.0	1128	1	T08322	insulin receptor s
1338	72	4.0	844	2	T37690	hypothetical prote	1411	71.5	4.0	1231	2	S30185	probable nuclear e
1339	72	4.0	844	2	T52396	formin-binding pro	1412	71.5	4.0	1250	2	T40062	CRAG protein - fru
1340	72	4.0	868	2	D86349	hypothetical prote	1413	71.5	4.0	1441	2	T13717	polyketide synthas
1341	72	4.0	878	1	RRXSIB	RNA-directed RNA p	1414	71.5	4.0	1446	2	S73013	Subtilase family p
1342	72	4.0	892	2	T06818	DNA topoisomerase	1415	71.5	4.0	1448	2	AI2007	WD-40 repeat prote
1343	72	4.0	984	2	C84781	hypothetical prote	1416	71.5	4.0	1526	2	AC2239	

1417 71.5 4.0 1540 2 H87203 polyketide synthas
1418 71.5 4.0 1592 2 S63208 hypohetical prote
1419 71.5 4.0 1603 1 VTKW5 vitellogenin vit-5
1420 71.5 4.0 1797 2 F69195 cell surface glyco
1421 71.5 4.0 2013 2 A11489 probable peptidogl
1422 71.5 4.0 2014 2 I36936 complement recepto
1423 71.5 4.0 2767 1 UIHU thyroglobulin prec
1424 71.5 4.0 3670 2 T36249 CDA peptide synthe
1425 71.5 4.0 4342 2 H83343 probable non-ribos
1426 71.5 4.0 5105 2 T32850 hypohetical prote
1427 71.5 4.0 6359 2 T31679 bacitracin synthe
1428 71.5 4.0 15281 2 S41309 cyclosporin synthe
1429 71 3.9 115 1 K3HUCI Ig kappa chain pre
1430 71 3.9 115 2 T27552 T-cell receptor be
1431 71 3.9 115 2 T12517 hypohetical prote
1432 71 3.9 128 2 S40373 Ig kappa chain - h
1433 71 3.9 128 2 A56701 Ig kappa chain v r
1434 71 3.9 128 2 A26406 Ig kappa chain v r
1435 71 3.9 131 2 B32513 Ig kappa chain prote
1436 71 3.9 133 2 E82603 hypohetical prote
1437 71 3.9 139 2 G32536 T-cell receptor al
1438 71 3.9 148 2 PH0116 Ig heavy chain pre
1439 71 3.9 197 2 T16627 hypohetical prote
1440 71 3.9 223 2 T09536 cytotoxic T-lympho
1441 71 3.9 224 2 F98215 transcription regu
1442 71 3.9 240 2 S06084 Ig kappa chain pre
1443 71 3.9 255 2 G83543 conserved hypohet
1444 71 3.9 261 2 AC0164 probable transport
1445 71 3.9 277 2 T37424 probable 31.5K pro
1446 71 3.9 313 2 A34677 secretory pathway
1447 71 3.9 319 2 B53290 oligopeptide trans
1448 71 3.9 323 2 B72224 conserved hypohet
1449 71 3.9 336 2 C83926 S-adenosylmethioni
1450 71 3.9 344 2 A69325 hypohetical prote
1451 71 3.9 356 2 T40041 hypohetical prote
1452 71 3.9 357 2 E86823 peptidoglycan synt
1453 71 3.9 368 2 G81289 UDPgalactopyranose
1454 71 3.9 375 2 H86938 conserved hypohet
1455 71 3.9 397 2 F96680 F5I14.10 (imported
1456 71 3.9 400 2 T34363 hypohetical prote
1457 71 3.9 404 2 AF2225 hypohetical prote
1458 71 3.9 405 1 VGBEGF glycoprotein G pre
1459 71 3.9 429 2 AC1163 flagellar hook-ass
1460 71 3.9 431 2 H81738 probable sodium-tr
1461 71 3.9 440 2 JL0144 interleukin-6 rece
1462 71 3.9 460 2 JL0145 interleukin-6 rece
1463 71 3.9 462 2 S74579 carboxyl-terminal
1464 71 3.9 472 2 AH3353 serine-type D-Ala-
1465 71 3.9 476 2 T19786 hypohetical prote
1466 71 3.9 478 2 H86100 hypohetical prote
1467 71 3.9 482 2 AC0426 serine-type D-Ala-
1468 71 3.9 501 2 T13316 hypohetical prote
1469 71 3.9 503 2 T40650 hypohetical prote
1470 71 3.9 507 2 J01929 phosphoprotein - r
1471 71 3.9 516 2 F82070 2-isopropylmalate
1472 71 3.9 522 2 E69116 conserved hypohet
1473 71 3.9 642 2 G69371 acetyl-CoA synthe
1474 71 3.9 646 2 T27899 hypohetical prote
1475 71 3.9 659 2 A85854 hypohetical prote
1476 71 3.9 660 2 AD0661 invasive-like prote
1477 71 3.9 695 2 S66662 protein-glutamine
1478 71 3.9 784 2 F97981 exoribonuclease R
1479 71 3.9 786 2 F95977 protein tyrosine k
1480 71 3.9 837 2 S43656 furin (EC 3.4.21.7
1481 71 3.9 848 2 T28055 hypohetical prote
1482 71 3.9 922 2 T40372 trp asp repeat pro
1483 71 3.9 946 1 A29550 methylenetetrahydr
1484 71 3.9 1015 2 S68141 nuclear protein HI
1485 71 3.9 1032 2 T23164 hypohetical prote
1486 71 3.9 1035 2 T23165 hypohetical prote
1487 71 3.9 1036 2 T05687 beta-galactosidase
1488 71 3.9 1057 2 T16676 hypohetical prote
1489 71 3.9 1081 2 T15692 hypohetical prote

1490 71 3.9 1144 2 A36968 Pl-like adhesin pr
1491 71 3.9 1145 2 T05573 hypohetical prote
1492 71 3.9 1152 2 AC1347 probable peptidogl
1493 71 3.9 1268 2 B99789 hemagglutinin/hemo
1494 71 3.9 1270 2 E85649 hypohetical prote
1495 71 3.9 1341 2 S09579 tail fiber protein
1496 71 3.9 1500 1 SYRTCA carbamoyl-phosphat
1497 71 3.9 1555 2 S38758 amylo-alpha-1,6-gl
1498 71 3.9 2062 2 G96602 probable receptor
1499 71 3.9 2163 2 S50675 pre-mRNA splicing
1500 71 3.9 2183 2 T42764 coagulation factor

ALIGNMENTS

RESULT 1

I56551

neurotrimin - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: I56551

R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L

J. Neurosci. 15, 2141-2156, 1995

A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed neu

A;Reference number: I56551; MUID:95198094; PMID:7891157

A;Accession: I56551

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-344 <RES>

A;Cross-references: UNIPROT:Q62718; UNIPARC:UPI00001305C7; EMBL:U16845; NID:G755184; PI

C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

Query Match 90.8%; Score 1639.5; DB 2; Length 344;

Best Local Similarity 92.9%; Pred. No. 1.3e-113; Indels 3; Gaps 1;

Matches 312; Conservative 9; Mismatches 12;

QY 12 ISWAIETGLAALCLF---QGVPRVSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVAV 68

Db 9 LPWKCLVVVSLRLFLVPTGVPVRSQDATFPKAMDNTVVRQGESATLRCTIDNRVTRVAV 68

QY 69 LNRSTILYAGNDKWCIDPRVLLSNTQVYSIEIQNVVDYDEGPTCVSDTNHPKTSRV 128

Db 69 LNRSTILYAGNDKWCIDPRVLLSNTQVYSIEIQNVVDYDEGPTCVSDTNHPKTSRV 128

QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPAKGVFVSEDEYLEI 188

Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPAKGVFVSEDEYLEI 188

QY 189 QGITRQSGDYECASNDVAAPVRRVKVTNVPYVISEAKGTGVPVQKGTLCQCEASAV 248

Db 189 QGITRQSGDYECASNDVAAPVRRVKVTNVPYVISEAKGTGVPVQKGTLCQCEASAV 248

QY 249 PSAEFQWYKDDKRLIEGKGVKVENRPFISKLIFNVSEHDYGNVYTCVANKLGHNTWASI 308

Db 249 PSAEFQWYKDDKRLIEGKGVKVENRPFISKLIFNVSEHDYGNVYTCVANKLGHNTWASI 308

QY 309 MLFGPGAVSEVNGTSRRAGCWWLLPLLVLLHLILKF 344

Db 309 MLFGPGAVSEVNGTSRRAGCWWLLPLLVLLHLILKF 344

RESULT 2

JC1238

opioioid-binding protein (clone DUZ1) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: JC1238

R;Lippman, D.A.; Lee, N.M.; Loh, H.H.

Gene 117, 249-254, 1992

A;Title: Opioioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain

A;Reference number: JC1238; MUID:92347701; PMID:11339369

A;Accession: JC1238

A:Molecule type: mRNA
A:Residues: 1-338 <LIP>
A:Cross-references: UNIPROT:P32736; UNIPARC:UPI000002B020; GB:M88709; NID:g203245; PIDN:
A:Experimental source: brain
C:Genetics:
A:Gene: OBCAM
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 71.2%; Score 1285.5; DB 2; Length 338;
Best Local Similarity 71.6%; Pred. No. 1.7e-87;
Matches 242; Conservative 35; Mismatches 60; Indels 1; Gaps 1;

QY 8 MHSISWALFTGLAALCLFGVVRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVA 67
DB 1 MHPAYWVFSATTALLFTPGVVRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVA 60

QY 68 WLNRSITLYAGNDKWCLDPRVLLSNTQYSEIQNVDDYDREGPYTCSVQTDNHPKTSR 127
DB 61 WLNRSITLYAGNDKWSIDPRVILVNTPTQYSIMIQNVDDYDREGPYTCSVQTDNHPKTSR 120

QY 128 VHLIVQSPKIVEISSDISINEGNISLTCTATGRPEPTVWRHISPK-AVGFSVSEDEYL 186
DB 121 VHLIVQPPQIMNISSDITVNEISSVTLLCLAIGRPEPTVWRHLSVKEGQGFVSEDEYL 180

QY 187 EIQGITREOSGDYECASNDVAAPVRRVKVTVNYPPYISEAKGTGVPVQKGTLOCEAS 246
DB 181 EISDIKRDQSGEYECASNDVAAPVRRVKVTVNYPPYISKAKNTGVSQKGLSCSEAS 240

QY 247 AVPSAEFQWKDKRLIEGKGVKVENRPFLLSKLIFPNVSEHDYGNVTCVASKLGHNTNA 306
DB 241 AVPMASEFQWKEDTRLATGLDGVRIENKGRISLTITFFNVSEKDYGNVTCVATNKLGNNTNA 300

QY 307 SITMFGPAGVSEVNSGTSRRAGCVWLLPLLVHLLKPF 344
DB 301 SITLYGPAVIDGVNSASRALACLWLSGTFFAHPFIKF 338

RESULT 3
JC4025
Oploid-binding cell adhesion protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C:Accession: JC4025
R:Shark, K.B.; Lee, N.M.
A:Title: Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a huma
A:Reference number: JC4025; MUID:95237612; PMID:7721093
A:Accession: JC4025
A:Molecule type: mRNA
A:Residues: 1-345 <SHA>
A:Cross-references: UNIPROT:Q14982; UNIPARC:UPI0000055AE0; GB:L34774; NID:g514373; PIDN:
A:Experimental source: brain
C:Comment: This protein binds oploid alkalooids in the presence of acidic lipids, exhibit
C:Genetics:
A:Gene: GDB:OPCML; OBCAM; OPCM
A:Cross-references: GDB:251677; OMIM:600632
A:Map position: lipr-11lgr
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 70.2%; Score 1268; DB 2; Length 345;
Best Local Similarity 71.2%; Pred. No. 3.4e-86;
Matches 240; Conservative 37; Mismatches 56; Indels 4; Gaps 2;

QY 12 ISWAIFTGLAALCLF---QGVVRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVA 68
DB 9 LPWKCLVWVSLRLFLVPTGVPVRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVA 68

QY 69 LNRSTILYAGNDKWCLDPRVLLSNTQYSEIQNVDDYDREGPYTCSVQTDNHPKTSRV 128
DB 69 LNRSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVDDYDREGPYTCSVQTDNHPKTSRV 128

QY 129 HLIVQSPKIVEISSDISINEGNISLTCTATGRPEPTVWRHISPK-AVGFSVSEDEYLE 187

DB 129 HLIVQPPQIMNISSDITVNEGSSVTLLCLAIGRPEPTVWRHLSVKEGQGFVSEDEYLE 188
QY 188 ICGITREOSGDYECASNDVAAPVRRVKVTVNYPPYISEAKGTGVPVQKGTLOCEASA 247
DB 189 ISDIKRDQSGEYECASALNDVAAPVRRVKVTVNYPPYISKAKNTGVSQKGLSCSEASA 248

QY 248 VPSAEFQWKDKRLIEGKGVKVENRPFLLSKLIFPNVSEHDYGNVTCVASKLGHNTNA 307
DB 249 VPMASEFQWKEDTRLATGLDGMRIENKGRMSLTITFFNVSEKDYGNVTCVATNKLGNNTNA 308

QY 308 IMLFGPAGVSEVNSGTSRRAGCVWLLPLLVHLLKPF 344
DB 309 ITLYGPAVIDGVNSASRALACLWLSGTLLAHPFIKF 345

RESULT 4
S03199
Oploid-binding protein OPCAM precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S03199
R:Schofield, P.R.; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S.; Le
EMBO J. 8, 489-495, 1989
A:Title: Molecular characterization of a new immunoglobulin superfamily protein with pot
A:Reference number: S03199; MUID:89251576; PMID:2721489
A:Accession: S03199
A:Molecule type: mRNA
A:Residues: 1-345 <SCH>
A:Cross-references: UNIPROT:P11834; UNIPARC:UPI0000055ADF; EMBL:X12672; NID:g585; PIDN:
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: transmembrane protein
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-345/Product: oploid-binding protein OPCAM #status predicted <MAT>

Query Match 70.1%; Score 1266; DB 2; Length 345;
Best Local Similarity 71.6%; Pred. No. 4.8e-86;
Matches 240; Conservative 34; Mismatches 57; Indels 4; Gaps 2;

QY 14 WAIFTGLAALCLF---QGVVRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVAMLN 70
DB 11 WKCLVWVSLRLFLVPTGVPVRSGDATFPKAMDNTVVRQGESATLRCTIDNRVTRVAMLN 70

QY 71 RSTILYAGNDKWCLDPRVLLSNTQYSEIQNVDDYDREGPYTCSVQTDNHPKTSRVHL 130
DB 71 RSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVDDYDREGPYTCSVQTDNHPKTSRVHL 130

QY 131 IVQVSPKIVEISSDISINEGNISLTCTATGRPEPTVWRHISPK-AVGFSVSEDEYLEIQ 189
DB 131 IVQVPPQIMNISSDITVNEGSSVTLLCLAIGRPEPTVWRHLSVKEGQGFVSEDEYLEIS 190

QY 190 GITREOSGDYECASNDVAAPVRRVKVTVNYPPYISEAKGTGVPVQKGTLOCEASAVP 249
DB 191 DIKRDQSGEYECASALNDVAAPVRRVKVTVNYPPYISKAKNTGVSQKGLSCSEASAVP 250

QY 250 SAEFQWKDKRLIEGKGVKVENRPFLLSKLIFPNVSEHDYGNVTCVASKLGHNTNASTM 309
DB 251 MAEFQWKEDTRLATGLDGMRIENKGHISTLTITFFNVSEKDYGNVTCVATNKLGNNTNAST 310

QY 310 LFGPAGVSEVNSGTSRRAGCVWLLPLLVHLLKPF 344
DB 311 LYGPAVIDGVNSASRALACLWLSGTLLAHPFIKF 345

RESULT 5
JC1239
Oploid-binding protein (clones SG8 and SG13) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: JC1239
R:Lippman, D.A.; Lee, N.M.; Loh, H.H.
Gene 117, 249-254, 1992
A:Title: Oploid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain
A:Reference number: JC1239; MUID:92347701; PMID:1339369

A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM b
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00384
A;Molecule type: DNA
A;Residues: 642-1115 <BAR>
A;Cross-references: UNIPARC:UPI0000174375; EMBL:X07195
R;Barthelme, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse.
A;Reference number: A28281; MUID:88247737; PMID:2454455
A;Accession: A28281
A;Molecule type: mRNA
A;Residues: 804-1081 <BA3>
A;Cross-references: UNIPARC:UPI000016CF42; EMBL:X07244; NID:g53321; PID:CAA30230.1; PID
R;Rougou, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
A;Cross-references: UNIPARC:UPI0000174376
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IDMS
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; su
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status exp
F;20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta
F;20-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;262-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: transmembrane #status predicted <TM>
F;730-1115/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 283.5; DB 1; Length 1115;
Best Local Similarity 25.8%; Pred. No. 7e-13;
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

QY 44 NVTVROGESATLRCTIDNRVTRVAVLNRSTLYAGNDKWCCLDPVVLNSNTQTQYSIEI 95
Db 222 NATANLQSVTLVCDAG-----RPEPTM-----SWTKDGEPIENEBEDRSRVS 268

QY 96 TQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNISL 155
Db 269 DSSEVTIRNVDRKDEAEYVCIAENKAGEQDASHLKVPAPKITYVENQTAMLEEQVTL 328

QY 156 TCATGRPEPTVTR-----HISPKAVGFVSEDEYLEIQITREQSGDYE 200
Db 329 TCASAGDPIPSITWRTSTRNISSEEQDLGHWVVRSHARVSS---LTKSIQVRDAGEYM 385

QY 201 CSASNDVAAPVRRVKVTVNYPPIYISBAKGTGVPVGQKGLQCEASAVPSAEFQWKDDK 260
Db 386 CTASNTIGQP-SQSIDLEFOYAPKLGQPVAVYTWEGNVNITCEVFAFPSATISWFRDQ 444

QY 261 RLIEGK-KGVKVENRPPLSKLIFPNVSEHDYGNVTCVASNKLGHNTASIML 310
Db 445 LLPSSNYSNLIKYNTPSASYLEVTPDSEDFGNVCTAVNRIGQESLEFIL 495

RESULT 11

JE0099
N;Alternate names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JE0099
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the m
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0099
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: UNIPROT:O73633; UNIPARC:UPI00000FBC8B; DDBJ:AB008162; NID:g3116226;
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through b
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 15.5%; Score 279.5; DB 2; Length 725;
Best Local Similarity 27.9%; Pred. No. 7.9e-13;
Matches 80; Conservative 50; Mismatches 120; Indels 37; Gaps 11;

QY 44 NVTVROGESATLRCTIDN-RVTRVAVLNRSTLYAGNDKWCCLDPVVLNSNTQTQYSIEI 102
Db 219 NATAKVAESVVLSCDADGFPDPEISWLKGEPIEDGEEK-----TSFNDQSEMTI 269

QY 103 QNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNISITCIATGR 162
Db 270 HHVEKDEAEYSCIANNQAGEAEATLLKVKYAKPKITYVENKTAV-ELDEITLTCBASGD 328

QY 163 PEPTVTW----RHISPAV---GFVSEDEYLEIQITRE-----QSGDVECSASNDVAAP 210
Db 329 PIPSITWRTAVNRNISSEATLTDGHIIVVKEHIRMALTLKDIOQVTDAGEYFCIASNPIGVD 388

QY 211 VVRVKVTVNYPPIYISBAKGTGVPV-----GQKGLQCEASAVPSAEFQWKDDKRLIE 264
Db 389 -MQMYFEVQYAPK---RG---PVVYTWEGNPVNITCEVFAHPRAAVTWFRDQGLLPS 441

QY 265 GK-KGVKVENRPPLSKLIFPNVSEHDYGNVTCVASNKLGHNTASIML 310
Db 442 SNFSNIKIYSGPTSSSLEVPDSEDFGNVCTAINTIGHFSEFIL 488

RESULT 12
IJCHNL
neural cell adhesion molecule long domain form precursor - chicken
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Gallus gallus (Chicken)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A43613; B43613; A25435; B25435; A46550; S36950; A44369; A60852; S29668
R;Cunningham, B.A.; Hemperly, J.J.; Murray, B.A.; Prediger, E.A.; Brackenbury, R.; Edel
Science 236, 799-806, 1987
A;Title: Neural cell adhesion molecule: structure, immunoglobulin-like domains, cell su
A;Reference number: A43613; MUID:87206190; PMID:3576199
A;Accession: A43613
A;Molecule type: mRNA
A;Residues: 1-175 <CU2>
A;Cross-references: UNIPROT:P13590; UNIPARC:UPI0000174387; GB:M15860
A;Accession: B43613
A;Molecule type: protein
A;Residues: 20-44;120-127;202-221;320-342;399-415;640-659;822-828 <CUN>
A;Cross-references: UNIPARC:UPI0000174388; UNIPARC:UPI0000174389; UNIPARC:UPI0000174384
A;Note: Asn-222 probably binds carbohydrate; Asn-226 probably does not
R;Hemperly, J.J.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986
A;Title: Sequence of a cDNA clone encoding the polystylastic acid-rich and cytoplasmic dom
A;Reference number: A25435; MUID:86206089; PMID:3458261
A;Accession: A25435

A:Molecule type: mRNA
A:Residues: 128-1091 <HEM>
A:Cross-references: UNIPARC:UPI000017438F; GB:M13210
A:Accession: B25435
A:Molecule type: protein
A:Residues: 128-140;222-240;428-439;611-631;744-760;763-781;1080-1084 <HE2>
A:Cross-references: UNIPARC:UPI0000174390; UNIPARC:UPI0000174391; UNIPARC:UPI0000174392;
R:Murray, B.A.; Owens, G.C.; Prediger, E.A.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.
J. Cell Biol. 103, 1431-1439, 1986
A:Title: Cell surface modulation of the neural cell adhesion molecule resulting from alb
A:Reference number: A46550; MUID:87033934; PMID:3771645
A:Accession: A46550
A:Molecule type: DNA
A:Residues: 810-1070 <MUR>
A:Cross-references: UNIPARC:UPI0000174397; GB:X04479
R:Sasner, M.; Covault, J.
submitted to the EMBL Data Library, February 1993
A:Reference number: S36950
A:Accession: S36950
A:Molecule type: DNA
A:Residues: 1-17 <SAS>
A:Cross-references: UNIPARC:UPI0000171377; EMBL:X70342; NID:G417631; PIDN:CAA49807.1; PI
R:Colwell, G.; Li, B.; Forrest, D.; Brackenbury, R.
Genomics 14, 875-882, 1992
A:Title: Conserved regulatory elements in the promoter region of the N-CAM gene.
A:Reference number: A44369; MUID:93122757; PMID:1478668
A:Accession: A44369
A:Molecule type: DNA
A:Residues: 1-17 <COF>
A:Cross-references: UNIPARC:UPI0000171377; EMBL:Z12128; NID:G63653; PIDN:CAA78113.1; PID
A:Experimental source: White Leghorn
R:Cole, G.J.; Loewy, A.; Cross, N.V.; Akeson, R.; Glaeser, L.
J. Cell Biol. 103, 1739-1744, 1986
A:Title: Topographic localization of the heparin-binding domain of the neural cell adhes
A:Reference number: A60852; MUID:87057627; PMID:2430978
A:Accession: A60852
A:Molecule type: protein
A:Residues: 20-29 <COL>
A:Cross-references: UNIPARC:UPI0000174398
R: Rao, Y.; Wu, X.F.; Gariepy, J.; Rutishauser, U.; Siu, C.H.
J. Cell Biol. 118, 937-949, 1992
A:Title: Identification of a peptide sequence involved in homophilic binding in the neur
A:Reference number: A43280; MUID:92363934; PMID:1380002
A:Comment: annotation; homophilic binding region
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; ei
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1091/Product: neural cell adhesion molecule, long domain form #status experimental
F:20-809,1071-1091/Product: neural cell adhesion molecule, short domain form #status exp
F:20-711/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-289/Domain: immunoglobulin homology <IMM3>
F:262-271/Region: NCAM binding #status experimental
F:322-387/Domain: immunoglobulin homology <IMM4>
F:419-481/Domain: immunoglobulin homology <IMM5>
F:518-595/Domain: fibronectin type III repeat homology <FN3A>
F:624-685/Domain: fibronectin type III repeat homology <FN3B>
F:712-729/Domain: transmembrane #status predicted <TM>
F:730-1091/Domain: intracellular #status predicted <INT>
F:41-96,139-189,235-287,329-385,426-479/Disulfide bonds: #status predicted
F:222/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:315,347,423,449,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.5%; Score 279.5; DB 1; Length 1091;
Best Local Similarity 26.0%; Pred. No. 1.3e-12;
Matches 78; Conservative 52; Mismatches 131; Indels 39; Gaps 9;
31 VRSGDATFPKAMDNVTRQGESATLRCTIDNRVTRVAVLNRSTILYAGNDKWLCDPRVVL 90

Db 214 VRARQSTM-----NATANLSQSVTLACDADG-----FPEPTM-----TWTKGEPTIE 255
QY 91 LSNQTQYSIE-----IQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISS 143
Db 256 QEDNEEKYSFNVDGSELIIKKYDKSDEAIEYICIAENKAGEQDATIHLKVFAPKPIYVEN 315
QY 144 DISINEGNNISITCTATGRPEPTVM---RHISPKAV---GFVSEDEVELEIQITREQ- 195
Db 316 KTAMELEQITLTCESAGDPIPSITWKTSTRNISNEEKTLDGRIVRVSHARVSSLTKEI 375
QY 196 ----SGDYECASNDDVAAPVVRVRKVTVNYPPISEAKGTGVPVGQKGTLOCEASAVPSA 251
Db 376 QYTDAGEVCTASNTIGQD-SQAMYLEVOYAPKLOGPVAVYTWEGNQNVIITCEVAYPSA 434
QY 252 EFQWYKDDKRLIEGK-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIML 310
Db 435 VISWFRDQGLLPSSNYSNIKIYNTPSASYLEVTPDSENDGNYNCTAVNRIGQESSEFIL 494
RESULT 13
T42633
connectin/titin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42633
R:Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin r
A:Reference number: 222221; MUID:96254045; PMID:8660363
A:Accession: T42633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4162 <YAJ>
A:Cross-references: UNIPROT:Q98918; UNIPARC:UPI000011025A; EMBL:D83390; NID:G1513029; P
A:Experimental source: breast muscle
C:Keywords: skeletal muscle
Query Match 15.4%; Score 278.5; DB 2; Length 4162;
Best Local Similarity 27.3%; Pred. No. 8.7e-12;
Matches 78; Conservative 38; Mismatches 145; Indels 25; Gaps 7;
37 TFPKAMDNVTRQGESATLRCTI-DNRVTRVAVLNRSTILYAGNDKWLCDPRVLLSNQ 95
3747 SFVKPEPFNVLSGENITFTSIVKSGPPELVKFRGSIELAPGK-----CNT 3795
QY 96 TQYSI---EIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNN 152
Db 3796 LQDSVAELELFDVQPLQSGDYTCQVSNBAGKISCTTTLFVKPEPAKFMKVNLDLSVEKGN 3855
QY 153 ISLTCTIATGRPEPTVM-----RHISPKAVGFVSEDEYLBIOGITRQSGDYECASN 205
Db 3856 LILECTYGTGTPPISVTVKKNKGVILKHSEKCSITTTTETSAILEIPNKLDEQDQYSCHIEN 3915
QY 206 DVAAFPVVRVKVTVNYPY-ISEAKGTGVPVGQKGTLOCEASAVPSAEQWVKDDKRLIE 264
Db 3916 DSGQDNCHGA-ITILEPPYFVTPLEPVQVTVGDSASLQCVAGTPEMIVSWYKGDTKL-R 3973
QY 265 GKKGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIML 310
Db 3974 GTATVKMHFKNQVATLVFSQVSDSDSGEYICKVENTVGEATSSLL 4019
RESULT 14
IURTNC
neural cell adhesion molecule short domain form precursor - rat
N:Alternate names: NCAM-140
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
A:Accession: S00846; B37795; I58136
R:Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A:Title: Identification of a cDNA clone that contains the complete coding sequence for

A;Reference number: S00846; MUID:88059265; PMID:3680385
A;Accession: S00846
A;Molecule type: mRNA
A;Residues: 1-858 <SMA>
A;Cross-references: UNIPROT:P13596; UNIPARC:UPI0000174378; EMBL:X06564
R;Small, S.J.; Akeson, R.
J. Cell Biol. 111, 2089-2096, 1990
A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A;Reference number: A37795; MUID:91035620; PMID:1699951
A;Accession: B37795
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 340-381 <SM2>
A;Cross-references: UNIPARC:UPI0000174379
R;Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: I58136; MUID:90166485; PMID:2483093
A;Accession: I58136
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 355-364 <RES>
A;Cross-references: UNIPARC:UPI00000066F; GB:M32611; NID:G205643; PIDN:AAA41679.1; PID:
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <M
F;20-721/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-398/Domain: immunoglobulin homology <IMM4>
F;430-492/Domain: immunoglobulin homology <IMM5>
F;529-606/Domain: fibronectin type III repeat homology <FN3A>
F;635-695/Domain: fibronectin type III repeat homology <FN3B>
F;722-739/Domain: transmembrane #status predicted <TM>
F;740-858/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-396,437-490/Diulfide bonds: #status predicted
F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.4%; Score 277.5; DB 1; Length 858;
Best Local Similarity 25.3%; Pred. No. 1.4e-12;
Matches 75; Conservative 50; Mismatches 132; Indels 37; Gaps 7;

QY 44 NVTVROGESATLRCTIDN-RVTRVAVLNSTILYAGNDKWCLDPRVLLSNTQTSIEI 102
Db 222 NATANLQGSVTLVCDADGPFPTMSWTKGEPTEENEBE-----DDEKHIFSDSSSE--LTI 275

QY 103 QNVVDVDEGPYTCVOTDNHPTKTSRVHLIVQVSPKIVEISSDISINEGNISLTCTATGR 162
Db 276 RVNDKNDKAEYVCIENKAGEQDASHLKVPKPKITYVENQVAMELEEQVLTTCASGD 335

QY 163 PEPTVTWR-----HISPKAVGFVSEDEYLEIQGITREQSG 197
Db 336 PIPSITWRTTSTRNISSEKASWTRPEKETLDGHVVRSHARVSS---LTLKSIQYTDAG 392

QY 198 DYECASNDVAAPVRRVKVTVPYVISEAKGTGVPVQKGLTQCEASAVPSAEQVYWK 257
Db 393 EYICTASNTIQD--SQSMYLEQVYAPKLGFPVAVYTWEGNQVNITCEVFAYPSATISWFR 451

QY 258 DDKRLIBGK-KGVKVENRPFLSKLIFPNVSEHDYGNVTCVASKLGHWTNASIML 310
Db 452 DGQLPSSNYSNIKINYTPSASYLEVTPDSENDFGNCTAVNRIGQESLEFIL 505

RESULT 15

IJXLNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain f
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 <KRI>
A;Cross-references: UNIPROT:P16170; UNIPARC:UPI000013FDC5; EMBL:M25696; NID:G214609; P
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mo
C;Comment: Several forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <L
F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pr
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Diulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.4%; Score 277.5; DB 1; Length 1088;
Best Local Similarity 27.9%; Pred. No. 1.9e-12;
Matches 80; Conservative 49; Mismatches 121; Indels 37; Gaps 11;

QY 44 NVTVROGESATLRCTIDN-RVTRVAVLNSTILYAGNDKWCLDPRVLLSNTQTSIEI 102
Db 219 NATANNAESVVLSCDADGPFDPPEISLWKKGPEIDGEEK-----ISFNDQSEMTI 269

QY 103 QNVVDVDEGPYTCVOTDNHPTKTSRVHLIVQVSPKIVEISSDISINEGNISLTCTATGR 162
Db 270 HHVKDDEAEYS CIANNQAGEAEATILLKVKPKITYVENKTAV-ELDEITLTCASGD 328

QY 163 PEPTVTW----RHISPKAV---GFVSEDEYLEIQGITRE-----QSGDYECASNDVAAP 210
Db 329 PIPSITWRTAVNRNISSEATLTDGHIIVVKGHIRMSALTLDKDIQYTDAGEVFCIASNPIGVD 388

QY 211 VVRVKVTVPYVISEAKGTGVPV-----GQKGLTQCEASAVPSAEQVYKDDKRLIE 264
Db 389 -MQAMTFEVOYAPKI---RG---PVVYTWEGNPVNITCEVFAPRAAVTWFRDGLQLPS 441

QY 265 GK-KGVKVENRPFLSKLIFPNVSEHDYGNVTCVASKLGHWTNASIML 310
Db 442 SNFSNIIKISGPTSSSLEVNPDSENDFGNCTAINTIGHFSEFIL 488

Search completed: February 7, 2006, 16:48:18
Job time : 57 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: February 7, 2006, 16:42:57 ; Search time 251 Seconds
 (without alignments)
 966.939 Million cell updates/sec

Title: US-09-981-915A-523
 Perfect score: 1806
 Sequence: 1 MKTIQKMHNSWIAFTGL.....RRAGCVLLPLDLVLLHLKF 344

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 2166443| seqs, 705528306 residues
 Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : Uniprot 05.80.*
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1797	99.5	344	Q5R554_PONPY	Q5r554 pongo pygma
2	1780	98.6	344	Q8BG33_MOUSE	Q8bg33 m mus muscu
3	1665.5	92.2	344	1 NTRI_HUMAN	Q9p121 homo sapien
4	1647.5	91.2	344	1 NTRI_MOUSE	Q99p10 mus musculus
5	1639.5	90.8	344	1 NTRI_RAT	Q62718 rattus norv
6	1636	90.6	345	2 Q58DA5_BOVIN	Q58da5 bos taurus
7	1477.5	81.8	353	1 CEPUL_CHICK	Q90773 gallus gall
8	1428	79.1	313	2 Q57596_CHICK	Q57596 gallus gall
9	1427.5	79.0	344	2 Q93442_CHICK	Q93442 gallus gall
10	1357.5	75.2	315	2 Q9DGI5_CHICK	Q9dgi5 gallus gall
11	1306	72.3	337	2 Q6DFY2_MOUSE	Q6dfy2 mus musculus
12	1305	72.3	337	1 OBCAM_CHICK	Q98892 gallus gall
13	1295.5	71.7	338	2 Q7Z3W6_HUMAN	Q7z3w6 homo sapien
14	1295.5	71.7	338	2 Q5R7T4_PONPY	Q5r7t4 pongo pygma
15	1276.5	70.7	345	2 Q6GM08_XENLA	Q6gm08 xenopus lae
16	1275.5	70.6	344	2 Q9DF61_CHICK	Q9df61 gallus gall
17	1274	70.5	336	2 Q5ISA8_9PRIM	Q5isa8 saimiri bol
18	1270.5	70.3	344	2 Q6B014_HUMAN	Q6b014 homo sapien
19	1268	70.2	345	1 OPCM_HUMAN	Q14982 homo sapien
20	1268	70.2	345	1 OPCM_PANTR	Q5i651 pan troglod
21	1266	70.1	345	1 OPCM_BOVIN	F11834 bos taurus
22	1259	69.7	345	1 OPCM_RAT	F32736 rattus norv
23	1251.5	69.3	319	2 Q5ISM6_MACPA	Q5ism6 macaca fasc
24	993.5	55.0	342	2 Q642G9_BRARE	Q642g9 brachydanio
25	945	52.4	334	2 Q02870_CHICK	Q02870 gallus gall
26	938.5	52.0	338	1 LSAMP_CHICK	Q98919 gallus gall
27	931.5	51.6	338	1 LSAMP_HUMAN	Q13449 homo sapien
28	930.5	51.5	350	2 Q02869_CHICK	Q02869 gallus gall
29	926.5	51.3	338	1 LSAMP_RAT	Q62813 rattus norv
30	913	50.6	361	2 Q5M960_RAT	Q5m960 rattus norv
31	904	50.1	337	2 Q6GL27_XENLA	Q6gl27 xenopus lae

32	894	49.5	1 LSAMP_MOUSE	Q8b1k3 mus musculus
33	868	48.1	2 Q503N3_BRARE	Q503n3 brachydanio
34	842	46.6	2 Q9W6V2_CHICK	Q9w6v2 gallus gall
35	824	45.6	2 Q5R412_PONPY	Q5r412 pongo pygma
36	823	45.6	1 NEGR1_HUMAN	Q723b1 homo sapien
37	823	45.6	2 Q5VT21_HUMAN	Q5vt21 homo sapien
38	819	45.3	2 Q5R645_PONPY	Q5r645 pongo pygma
39	815	45.1	348 1 NEGR1_RAT	Q920j8 rattus norv
40	814	45.1	348 1 NEGR1_MOUSE	Q80z24 mus musculus
41	761	42.1	2 Q4SL89_TETNG	Q4sl89 tetraodon n
42	759	42.0	2 Q8HW98_MOUSE	Q8hw98 mus musculus
43	724.5	40.1	312 2 Q4SUX1_TETNG	Q4sux1 tetraodon n
44	686.5	38.0	2 Q8BMT5_MOUSE	Q8bmt5 m mus muscu
45	656.5	36.4	2 Q80T70_MOUSE	Q80t70 mus musculus
46	642	35.5	2 Q4SDU6_TETNG	Q4sdu6 tetraodon n
47	599	33.2	2 Q9W6V1_CHICK	Q9w6v1 gallus gall
48	545.5	30.2	2 Q8N440_HUMAN	Q8n440 homo sapien
49	518.5	28.7	2 Q568D3_BRARE	Q568d3 brachydanio
50	471.5	26.1	140 2 Q4SL88_TETNG	Q4sl88 tetraodon n
51	467.5	25.9	193 2 Q4S7M1_TETNG	Q4s7m1 tetraodon n
52	380.5	21.1	536 2 Q4V5E0_DROME	Q4v5e0 drosophila
53	380.5	21.1	606 2 Q9VMN6_DROME	Q9vmn6 drosophila
54	355	19.7	290 2 Q5TNT8_ANOGA	Q5tnt8 anopheles g
55	350.5	19.4	672 2 Q8IP70_DROME	Q8ip70 drosophila
56	349.5	19.4	532 2 Q6NNU3_DROME	Q6nnu3 drosophila
57	349.5	19.4	532 2 Q9VLF0_DROME	Q9vlf0 drosophila
58	348	19.3	554 2 Q9W4R3_DROME	Q9w4r3 drosophila
59	346	19.2	301 2 Q7Q864_ANOGA	Q7q864 anopheles g
60	340	18.8	299 2 Q7Q0P9_ANOGA	Q7q0p9 anopheles g
61	338.5	18.7	413 2 Q4V3F0_DROME	Q4v3f0 drosophila
62	338	18.7	376 2 Q9VMB2_DROME	Q9vmb2 drosophila
63	333	18.4	315 2 Q5TQN9_ANOGA	Q5tqn9 anopheles g
64	332.5	18.4	317 2 Q7Q863_ANOGA	Q7q863 anopheles g
65	313.5	17.4	308 2 Q7Q863_ANOGA	Q7q863 anopheles g
66	313	17.3	550 2 Q9VMN9_DROME	Q9vmn9 drosophila
67	312.5	17.3	351 2 Q7Q0P8_ANOGA	Q7q0p8 anopheles g
68	308.5	17.1	528 2 P91670_DROME	P91670 drosophila
69	308	17.1	405 2 Q7PRJ5_ANOGA	Q7prj5 anopheles g
70	306	16.9	545 2 Q9VCT4_DROME	Q9vct4 drosophila
71	303.5	16.8	316 2 Q8WPB3_DROSI	Q8wpb3 drosophila
72	300.5	16.6	316 2 Q8WP94_DROSI	Q8wp94 drosophila
73	300	16.6	948 2 Q9VME2_DROME	Q9vme2 drosophila
74	298	16.5	302 2 Q7PN14_ANOGA	Q7pn14 anopheles g
75	297.5	16.5	316 2 Q8WP58_DROSI	Q8wp58 drosophila
76	297.5	16.5	333 1 AMAL_DROME	P15364 drosophila
77	297.5	16.5	341 2 Q7KSX2_DROME	Q7ksx2 drosophila
78	292.5	16.2	333 2 Q7PXA4_ANOGA	Q7pxa4 anopheles g
79	290.5	16.1	2673 2 Q96SC3_HUMAN	Q96sc3 homo sapien
80	290.5	16.1	5636 2 Q96RW7_HUMAN	Q96rw7 homo sapien
81	288.5	16.0	5635 2 Q5TVR7_HUMAN	Q5tvr7 homo sapien
82	287	15.9	846 2 Q57577_CYNPY	Q57577 cynops pyrr
83	287	15.9	1100 2 Q57576_CYNPY	Q57576 cynops pyrr
84	285.5	15.8	603 2 Q9NKF5_DROME	Q9nkf5 drosophila
85	284	15.7	403 2 Q9VP08_DROME	Q9vp08 drosophila
86	283.5	15.7	725 1 NCA11_MOUSE	P13594 mus musculus
87	283.5	15.7	1115 1 NCA11_MOUSE	P13594 mus musculus
88	282.5	15.6	605 2 Q921P2_MOUSE	Q921p2 mus musculus
89	282.5	15.6	838 2 Q8BQ96_MOUSE	Q8bq96 mus musculus
90	282.5	15.6	838 2 Q8C4B2_MOUSE	Q8c4b2 mus musculus
91	280.5	15.5	843 2 Q5EA96_BOVIN	Q5ea96 bos taurus
92	279.5	15.5	725 2 Q512D5_CANPA	O512d5 canis famil
93	279.5	15.5	725 2 Q73633_XENLA	Q73633 xenopus lae
94	279.5	15.5	847 2 Q512D7_CANPA	Q512d7 canis famil
95	279.5	15.5	1091 1 NCAM1_CHICK	P13590 gallus gall
96	278.5	15.4	4162 2 Q98918_CHICK	Q98918 gallus gall
97	277.5	15.4	719 2 Q661V0_XENLA	Q661v0 xenopus lae
98	277.5	15.4	858 1 NCAM1_RAT	P13596 rattus norv
99	277.5	15.4	1088 1 NCA11_XENLA	P16170 xenopus lae
100	276.5	15.3	405 2 Q6PFK4_BRARE	Q6pfk4 brachydanio
101	276	15.3	690 2 Q5ISL0_MACPA	Q5isl0 macaca fasc
102	276	15.3	761 1 NCA12_HUMAN	P13592 homo sapien
103	276	15.3	807 2 Q59FL7_HUMAN	Q59fl7 homo sapien
104	276	15.3	848 1 NCA11_HUMAN	P13591 homo sapien

105	275.5	15.3	846	2	Q5RIQ0_FELCA	Q5RIQ0 felis silve	178	243.5	13.5	1021	1	CNTN1_RAT	Q63198 rattus norv
106	275.5	15.3	847	2	Q5G7G8_FELCA	Q5G7G8 felis silve	179	243.5	13.5	1036	1	CNTN2_CHICK	P28685 gallus gall
107	275.5	15.3	853	1	NCAM1_BOVIN	P31836 bos taurus	180	243.5	13.5	1278	2	Q4RRSE_TETNG	Q4rr85 tetraodon n
108	274.5	15.2	857	2	Q512D6_CANPA	Q512d6 canis famli	181	243	13.5	223	2	Q7QCH7_ANOGA	Q7qch7 anopheles g
109	273.5	15.1	725	2	Q73634_XENLA	Q73634 xenopus lae	182	242.5	13.4	949	1	MAMC1_RAT	P60756 rattus norv
110	273	15.1	349	2	Q5TS39_ANOGA	Q5ts39 anopheles g	183	241.5	13.4	837	1	NCAM2_HUMAN	O15394 homo sapien
111	273	15.1	423	2	Q6DJB3_XENTR	Q6djb3 xenopus tro	184	241.5	13.4	1018	1	CNTN1_BOVIN	Q28106 bos taurus
112	272.5	15.1	1333	2	Q08476_CHICK	Q08476 gallus gall	185	241.5	13.4	1020	1	CNTN1_MOUSE	P12960 mus musculu
113	271	15.0	858	2	Q86X47_HUMAN	Q86x47 homo sapien	186	241	13.3	1100	2	Q5RKM8_MOUSE	Q5rkm8 mus musculu
114	270.5	15.0	1092	1	NCAL12_XENLA	P36335 xenopus lae	187	240.5	13.3	1693	2	Q7QCU0_ANOGA	Q7qcu0 anopheles g
115	270	15.0	1479	2	Q7KQT5_DROME	Q7kqt5 drosophila	188	240	13.3	843	2	Q4S6A5_TETNG	Q4s6a5 tetraodon n
116	269.5	14.9	484	2	Q26475_SCHAM	Q26475 schistocerc	189	240	13.3	3707	1	PGBM_MOUSE	Q05793 mus musculu
117	268.5	14.9	722	2	Q4KMG2_HUMAN	Q4kmg2 homo sapien	190	239	13.2	2528	2	Q4S2G3_TETNG	Q4s2g3 tetraodon n
118	268.5	14.9	1496	2	Q92626_HUMAN	Q92626 homo sapien	191	237.5	13.2	1054	1	LRIG2_MOUSE	Q52kr2 mus musculu
119	268	14.8	1460	2	Q5HZ61_XENTR	Q5hz61 xenopus tro	192	237	13.1	312	2	Q66KV0_XENLA	Q66kv0 xenopus lae
120	268	14.8	5533	2	Q5RIP6_BRARE	Q5rip6 brachydanio	193	236.5	13.1	409	2	Q4SFV2_TETNG	Q4sfv2 tetraodon n
121	265	14.7	1482	2	Q7V4Y0_DROME	Q7v4y0 drosophila	194	235.5	13.0	632	2	Q6ZRK5_HUMAN	Q6zrk5 homo sapien
122	264.5	14.6	943	2	Q7PRK4_ANOGA	Q7prk4 anopheles g	195	235.5	13.0	1027	1	CNTN5_CHICK	Q90w79 gallus gall
123	263.5	14.6	323	2	Q7QBA7_ANOGA	Q7qba7 anopheles g	196	235.5	13.0	2623	2	Q6WRI0_HUMAN	Q6wri0 homo sapien
124	263	14.6	1431	2	Q80U60_MOUSE	Q80u60 mus musculu	197	235.5	13.0	2752	2	Q7QKD0_ANOGA	Q7qkd0 anopheles g
125	263	14.6	3950	2	Q7VRFS_CANPA	Q7yrf5 canis famli	198	234.5	13.0	358	2	Q90490_BRARE	Q90490 brachydanio
126	262.5	14.5	829	2	Q4RIG0_TETNG	Q4rig0 tetraodon n	199	234.5	13.0	557	2	Q4RB52_TETNG	Q4rb52 tetraodon n
127	261.5	14.5	437	2	Q8IZP8_HUMAN	Q8izp8 homo sapien	200	234.5	13.0	779	2	O97136_MANSE	O97136 manduca sex
128	261.5	14.5	1010	1	CNTN1_CHICK	P14781 gallus gall	201	234.5	13.0	837	2	O97137_MANSE	O97137 manduca sex
129	261	14.5	1031	2	Q90YM2_BRARE	Q90ym2 brachydanio	202	234.5	13.0	1040	1	CNTN2_RAT	P22063 rattus norv
130	261	14.5	1395	2	Q44924_DROME	Q44924 drosophila	203	234	13.0	1133	2	Q4T6R5_TETNG	Q4t6r5 tetraodon n
131	261	14.5	3410	2	Q7TN00_RAT	Q7tn00 rattus norv	204	233.5	12.9	1100	1	CNTN5_HUMAN	O94779 homo sapien
132	260.5	14.4	400	2	Q7P2S8_ANOGA	Q7p2s8 anopheles g	205	233	12.9	394	2	Q7ZXX1_XENLA	Q7zxx1 xenopus lae
133	260.5	14.4	500	2	Q9XZB7_DROME	Q9xzB7 drosophila	206	233	12.9	1028	1	CNTN6_RAT	P97528 rattus norv
134	260.5	14.4	500	2	Q9W260_DROME	Q9w260 drosophila	207	233	12.9	1049	2	Q4RVM2_TETNG	Q4rvM2 tetraodon n
135	260.5	14.4	862	2	Q4SST3_TETNG	Q4sst3 tetraodon n	208	232.5	12.9	1702	2	Q4RJ21_TETNG	Q4rj21 tetraodon n
136	260	14.4	601	2	Q96CJ3_HUMAN	Q96cj3 homo sapien	209	232.5	12.9	2693	2	Q8ISF3_CAEL	Q8laf3 caenorhabdi
137	260	14.4	1395	2	Q7RKV3_DROME	Q7rkV3 drosophila	210	232.5	12.9	2708	2	Q8ISF4_CAEL	Q8laf4 caenorhabdi
138	259	14.3	1429	2	Q9W213_DROME	Q10465 homo sapien	211	232.5	12.9	18519	2	Q8ISF6_CAEL	Q8laf6 caenorhabdi
139	259	14.3	7962	2	Q10465_HUMAN	Q10465 homo sapien	212	232.5	12.9	18534	2	Q8ISF7_CAEL	Q8laf7 caenorhabdi
140	259	14.3	34350	2	Q8WZ42_HUMAN	Q8wz42 homo sapien	213	231.5	12.8	858	2	O18466_HIRME	O18466 hirudo medi
141	258.5	14.3	395	2	Q8BZP4_MOUSE	Q8bzp4 mus musculu	214	231.5	12.8	1005	2	P79921_XENLA	P79921 xenopus lae
142	258.5	14.3	395	2	Q8BXJ7_MOUSE	Q8bxj7 m mus muscu	215	231.5	12.8	1379	2	Q4SMF3_TETNG	Q4smf3 tetraodon n
143	258.5	14.3	404	2	Q8BYP1_MOUSE	Q8byp1 mus musculu	216	231.5	12.8	5505	2	Q4RU89_TETNG	Q4ru89 tetraodon n
144	258.5	14.3	404	2	Q8BLQ9_MOUSE	Q8blq9 mus musculu	217	231	12.8	703	2	Q21139_CAEL	Q21139 caenorhabdi
145	257	14.2	1056	1	CNTN5_BRARE	Q7zw34 brachydanio	218	231	12.8	1028	1	CNTN6_HUMAN	Q6ny23 homo sapien
146	256	14.2	435	2	Q8N3J6_HUMAN	Q8n3j6 homo sapien	219	230.5	12.8	868	1	Q6NY23_BRARE	Q6ny23 brachydanio
147	255.5	14.1	265	2	Q4V3R1_DROME	Q4v3r1 drosophila	220	230.5	12.8	868	1	MUSK_RAT	Q82838 rattus norv
148	255.5	14.1	938	2	Q90YM1_BRARE	Q90ym1 brachydanio	221	230.5	12.8	1032	2	Q8UVD6_BRARE	Q8uvd6 brachydanio
149	255	14.1	359	1	LACH_DROME	Q24372 drosophila	222	230.5	12.8	1040	1	CNTN2_MOUSE	Q61330 mus musculu
150	254.5	14.1	5175	2	Q81OL3_CAEL	Q81ol3 caenorhabdi	223	230	12.7	1028	2	QSR6D4_PONPY	Q5rtd4 pongo pygma
151	254.5	14.1	5198	2	Q76518_CAEL	Q76518 caenorhabdi	224	229.5	12.7	510	2	Q801V8_BRARE	Q801v8 brachydanio
152	251.5	13.9	837	1	NCAM2_MOUSE	Q35136 mus musculu	225	229.5	12.7	867	2	Q5VZW7_HUMAN	Q5vzw7 homo sapien
153	250.5	13.9	377	2	O5TNT5_ANOGA	Q5tnt9 anopheles g	226	229.5	12.7	869	1	MUSK_HUMAN	O15146 homo sapien
154	250.5	13.9	1040	2	Q5RDT8_PONPY	Q5rtd8 pongo pygma	227	229.5	12.7	875	2	Q5VZW8_HUMAN	Q5vzw8 homo sapien
155	250.5	13.9	1342	2	Q9GPP6_DROME	Q9gpp6 drosophila	228	229	12.7	1056	2	Q90Z03_XENLA	Q90z03 xenopus lae
156	250.5	13.9	1342	2	Q9VYZ7_DROME	Q9vyz7 drosophila	229	229	12.7	2331	2	Q59EG0_HUMAN	Q59ego homo sapien
157	250	13.8	349	1	LACH_SCHAM	Q26474 schistocerc	230	229	12.7	4391	1	PGBM_HUMAN	P98160 homo sapien
158	250	13.8	795	2	Q90YM0_BRARE	Q90ym0 brachydanio	231	229	12.7	4391	2	Q5VU27_HUMAN	Q5vu27 homo sapien
159	250	13.8	955	1	MDGA1_HUMAN	Q8nf04 homo sapien	232	228.5	12.7	1040	1	Q9W675_BRARE	Q9w675 brachydanio
160	250	13.8	957	2	Q5TFS8_HUMAN	Q5tf88 homo sapien	233	228.5	12.7	1117	1	LRIG3_MOUSE	Q6pic6 mus musculu
161	249.5	13.8	1040	1	CNTN2_HUMAN	Q5t568 homo sapien	234	228	12.6	900	2	Q4SR23_TETNG	Q4sr23 tetraodon n
162	249.5	13.8	1040	2	Q5T054_HUMAN	Q5t046 homo sapien	235	228	12.6	1028	1	CNTN6_MOUSE	Q9jmb8 mus musculu
163	247	13.7	204	2	Q7PUY5_ANOGA	Q7pyu5 anopheles g	236	228	12.6	1409	2	Q617L8_CAEL	Q617l8 caenorhabdi
164	246.5	13.6	627	2	Q5RDU0_PONPY	Q5rdu0 pongo pygma	237	227.5	12.6	1051	1	PTK7_CHICK	Q91048 gallus gall
165	246.5	13.6	727	2	Q6RKB2_RAT	Q6rkb2 rattus norv	238	227.5	12.6	1099	1	CNTN5_RAT	P97527 rattus norv
166	246.5	13.6	837	2	Q6RKB3_RAT	Q6rkb3 rattus norv	239	227	12.6	633	2	Q5W431_BRARE	Q5w434 brachydanio
167	246.5	13.6	865	2	Q6BDA2_HUMAN	Q6bda2 homo sapien	240	227	12.6	651	2	Q5W433_BRARE	Q5w433 brachydanio
168	246.5	13.6	1018	1	CNTN1_HUMAN	Q12860 homo sapien	241	227	12.6	1189	2	Q9P2J2_HUMAN	Q9p2j2 homo sapien
169	245.5	13.6	292	2	Q4RFQ9_TETNG	Q4rfq9 tetraodon n	242	226.5	12.5	476	2	Q6AYP5_RAT	Q6ayp5 rattus norv
170	245.5	13.6	1033	2	Q4SBZ7_TETNG	Q4sbz7 tetraodon n	243	226.5	12.5	699	2	Q622N7_CAEL	Q622n7 caenorhabdi
171	245.5	13.6	1065	1	LRIG2_HUMAN	Q94898 homo sapien	244	226	12.5	5992	2	Q5W615_CAEL	Q5w615 caenorhabdi
172	245	13.6	1028	2	Q6INB5_XENLA	Q6inb5 xenopus lae	245	226	12.5	6632	1	UNC89_CAEL	Q01761 caenorhabdi
173	244.5	13.5	512	2	Q96DN8_HUMAN	Q96dn8 homo sapien	246	226	12.5	7122	2	Q5W616_CAEL	Q5w616 caenorhabdi
174	244.5	13.5	3493	2	Q4RJ20_TETNG	Q4rj20 tetraodon n	247	226	12.5	7441	2	Q5W617_CAEL	Q5w617 caenorhabdi
175	243.5	13.5	837	2	Q7Z7F2_HUMAN	Q7z7f2 homo sapien	248	226	12.5	8081	2	Q7Z120_CAEL	Q7z120 caenorhabdi
176	243.5	13.5	949	1	MAMC1_MOUSE	P60755 mus musculu	249	225.5	12.5	868	1	MUSK_MOUSE	Q61006 mus musculu
177	243.5	13.5	956	1	MAMC1_HUMAN	Q7z553 homo sapien	250	225.5	12.5	1070	2	Q4S2F2_TETNG	Q4s2f2 tetraodon n

251	225	12.5	881	2	Q4RQR3_TETNG	Q4RQR3 tetraodon n	324	215	11.9	1419	2	Q98SW3_BRARE	Q98SW3 brachydanio
252	224.5	12.4	1210	2	Q59FY0_HUMAN	Q59FY0 homo sapien	325	214.5	11.9	816	2	Q8NFA5_HUMAN	Q8NFA5 homo sapien
253	224.5	12.4	1224	2	Q00533_HUMAN	Q00533 homo sapien	326	214.5	11.9	1070	2	Q6IQ54_HUMAN	Q6IQ54 homo sapien
254	224	12.4	1119	1	LRIG3_HUMAN	Q6uxm1 homo sapien	327	214.5	11.9	1070	2	Q57650_HUMAN	Q57650 homo sapien
255	224	12.4	1252	2	Q96DN3_HUMAN	Q96dn3 homo sapien	328	214.5	11.9	1651	1	ROBO1_RAT	Q55005 rattus norv
256	223	12.3	417	2	Q5R6B7_PONPY	Q5r6b7 pongo pygma	329	214	11.8	545	2	Q7QIV4_ANOGA	Q7qiv4 anopheles g
257	223	12.3	417	2	Q7TNL1_MOUSE	Q7tnl1 mus musculus	330	214	11.8	920	2	Q4RSG7_TETNG	Q4rsg7 tetraodon n
258	222.5	12.3	595	2	Q5W431_FUGRU	Q5w431 fugu rubrip	331	214	11.8	1026	1	CNTN4_MOUSE	Q69226 mus musculu
259	222.5	12.3	630	2	Q5W436_FUGRU	Q5w436 fugu rubrip	332	213.5	11.8	398	2	Q8N126_HUMAN	Q8n126 homo sapien
260	222.5	12.3	648	2	Q5W435_FUGRU	Q5w435 fugu rubrip	333	213.5	11.8	875	2	Q4RRR9_TETNG	Q4rrr9 tetraodon n
261	222.5	12.3	838	2	Q4SP99_TETNG	Q4sp99 tetraodon n	334	213.5	11.8	1028	1	CNTN3_HUMAN	Q90232 homo sapien
262	222	12.3	450	2	Q6VR25_DROME	Q6vr25 drosophila	335	213.5	11.8	1389	2	Q90Z69_BRARE	Q90z69 brachydanio
263	222	12.3	595	2	Q6ZRS5_HUMAN	Q6zrs5 homo sapien	336	213	11.8	484	2	Q6BE00_XENLA	Q6be00 xenopus lae
264	221.5	12.3	773	2	Q59FV9_HUMAN	Q59fv9 homo sapien	337	213	11.8	1134	2	Q71B05_BRARE	Q71b05 brachydanio
265	221.5	12.3	862	1	CDD2_MOUSE	P35329 mus musculu	338	212.5	11.8	1264	2	P91767_MANSE	P91767 manduca sex
266	221	12.2	435	2	Q8WR44_CAEEL	Q8wr44 caenorhabdi	339	212	11.7	1026	1	CNTN4_RAT	Q62845 rattus norv
267	221	12.2	436	2	Q8MPV1_CAEEL	Q8mpv1 caenorhabdi	340	212	11.7	1089	2	Q4S556_TETNG	Q4s556 tetraodon n
268	221	12.2	1340	2	Q8NDA2_HUMAN	Q8nda2 homo sapien	341	212	11.7	1151	2	Q9QVN5_9MURI	Q9qvn5 rattus sp.
269	221	12.2	1746	2	Q8WY19_HUMAN	Q8wy19 homo sapien	342	211.5	11.7	773	2	Q61DE4_DROME	Q61de4 drosophila
270	221	12.2	1827	2	Q9VSG5_DROME	Q9vsg5 drosophila	343	211.5	11.7	873	1	FAS2_DROME	P34082 drosophila
271	221	12.2	2012	1	DSCAM_HUMAN	Q60469 homo sapien	344	211.5	11.7	1070	1	PTK7_HUMAN	Q13308 homo sapien
272	221	12.2	2023	2	Q59GH3_HUMAN	Q59gh3 homo sapien	345	211.5	11.7	1102	2	Q923W7_MOUSE	Q923w7 mus musculu
273	221	12.2	10495	2	Q4RE92_TETNG	Q4re92 tetraodon n	346	211.5	11.7	1109	2	Q8CE91_MOUSE	Q8ce91 mus musculu
274	220.5	12.2	333	2	Q8GBW8_HUMAN	Q8gbw8 homo sapien	347	211.5	11.7	1109	2	Q6AZB0_MOUSE	Q6azb0 mus musculu
275	220.5	12.2	336	2	Q9D6E7_MOUSE	Q9d6e7 mus musculu	348	211.5	11.7	1110	2	Q8CE73_MOUSE	Q8ce73 mus musculu
276	220.5	12.2	336	2	Q80VG4_MOUSE	Q80vg4 mus musculu	349	211.5	11.7	1461	1	NEO1_HUMAN	Q92859 homo sapien
277	220.5	12.2	428	2	Q6F3J3_MOUSE	Q6f3j3 mus musculu	350	211	11.7	349	2	Q7QJG1_ANOGA	Q7qjg1 anopheles g
278	220.5	12.2	443	2	Q8N2P4_HUMAN	Q8n2p4 homo sapien	351	211	11.7	377	2	Q4RZV7_TETNG	Q4rzv7 tetraodon n
279	220.5	12.2	445	2	Q8R4L1_MOUSE	Q8r4l1 mus musculu	352	211	11.7	396	2	Q99N28_MOUSE	Q99n28 homo sapien
280	220.5	12.2	445	2	Q8K3T6_MOUSE	Q8k3t6 mus musculu	353	211	11.7	1845	2	Q5MYA0_HUMAN	Q5mya0 homo sapien
281	220.5	12.2	456	2	Q8RSM8_MOUSE	Q8rsm8 mus musculu	354	211	11.7	6620	2	Q96AA2_HUMAN	Q96aa2 homo sapien
282	220.5	12.2	898	1	FAS2_SCHAM	P22648 schistocerc	355	211	11.7	6620	2	Q5VST9_HUMAN	Q5vst9 homo sapien
283	220.5	12.2	1095	2	Q58EP4_BRARE	Q58ep4 brachydanio	356	210	11.6	588	2	Q4RFF0_TETNG	Q4rff0 tetraodon n
284	220.5	12.2	1098	1	CNTN5_MOUSE	P68500 mus musculu	357	210	11.6	1561	2	Q924D2_MOUSE	Q924d2 mus musculu
285	220	12.2	1043	2	Q6PA07_XENLA	Q6pa07 xenopus lae	358	210	11.6	1730	2	Q7YRQ7_PIG	Q7yrq7 sus scrofa
286	220	12.2	1614	2	Q8UVD7_XENLA	Q8uvd7 xenopus lae	359	210	11.6	1914	1	MYLK_HUMAN	Q15746 homo sapien
287	219.5	12.2	330	2	Q90Z42_CHICK	Q90z42 gallus gall	360	210	11.6	1914	2	Q5MY99_HUMAN	Q5my99 homo sapien
288	219.5	12.2	390	2	Q66KX2_XENLA	Q66kx2 xenopus lae	361	210	11.6	1914	2	Q7Z4J0_HUMAN	Q7z4j0 homo sapien
289	219.5	12.2	442	2	Q9BY67_HUMAN	Q9by67 homo sapien	362	210	11.6	1949	2	Q6PDN3_MOUSE	Q6pdn3 mus musculu
290	219.5	12.2	1012	2	Q4SW91_TETNG	Q4sw91 tetraodon n	363	209.5	11.6	484	1	Q5QSL1_XENTR	Q5qsl1 xenopus tro
291	219	12.1	1089	2	Q5U3R8_BRARE	Q5u3r8 brachydanio	364	209	11.6	504	1	FGRL1_HUMAN	Q8n441 homo sapien
292	219	12.1	1009	2	Q93250_XENLA	Q93250 xenopus lae	365	209	11.6	1030	2	Q8NFA8_HUMAN	Q8nfa8 homo sapien
293	219	12.1	1026	1	CNTN4_HUMAN	Q8iwv2 homo sapien	366	209	11.6	1165	2	Q5T2F1_HUMAN	Q5t2f1 homo sapien
294	219	12.1	1062	2	Q8BKG3_MOUSE	Q8bkg3 mus musculu	367	209	11.6	1174	2	Q5T2F5_HUMAN	Q5t2f5 homo sapien
295	219	12.1	1091	1	LRIG1_MOUSE	P70193 mus musculu	368	209	11.6	2174	2	Q70BG7_ANOGA	Q70bg7 anopheles g
296	219	12.1	1093	1	LRIG1_HUMAN	Q96jai homo sapien	369	208.5	11.5	1028	1	CNTN3_MOUSE	Q70409 mus musculu
297	219	12.1	1093	1	Q5XWD3_HUMAN	Q5xwd3 homo sapien	370	208.5	11.5	1651	1	ROBO1_HUMAN	Q9y6n7 homo sapien
298	219	12.1	2222	2	Q4RY92_TETNG	Q4ry92 tetraodon n	371	208	11.5	1280	2	Q4RRJ3_TETNG	Q4rrj3 tetraodon n
299	219	12.1	4071	2	Q6KDZ1_CHICK	Q6kdz1 gallus gall	372	207.5	11.5	329	2	Q8N225_HUMAN	Q8n225 homo sapien
300	218.5	12.1	481	2	Q6OND3_CAEER	Q6ond3 caenorhabdi	373	207.5	11.5	1029	2	Q596X0_CARAU	Q596x0 carassius a
301	218.5	12.1	1114	2	Q9BKV1_HUMAN	Q9bkv1 homo sapien	374	207	11.5	452	2	Q5WRR1_CAEEL	Q5wrr1 caenorhabdi
302	218.5	12.1	1115	2	Q6UXJ5_HUMAN	Q6uxj5 homo sapien	375	207	11.5	600	2	Q8N7W7_HUMAN	Q8n7w7 homo sapien
303	218.5	12.1	1612	1	ROBO1_MOUSE	Q89026 mus musculu	376	207	11.5	1450	2	Q4SCT9_TETNG	Q4sct9 tetraodon n
304	218	12.1	2013	2	Q8VHZ8_RAT	Q8vhz8 rattus norv	377	206.5	11.4	915	2	Q8R4B3_MOUSE	Q8r4b3 mus musculu
305	218	12.1	2013	2	Q9RCE8_MOUSE	Q9rc8 mus musculu	378	206.5	11.4	952	2	Q4SPY1_TETNG	Q4spy1 tetraodon n
306	217.5	12.0	348	2	Q00557_HUMAN	Q00557 homo sapien	379	206.5	11.4	1098	2	Q4RRT1_TETNG	Q4rrt1 tetraodon n
307	217.5	12.0	626	2	Q4SM56_TETNG	Q4sm56 tetraodon n	380	206.5	11.4	2016	2	Q9NBA1_DROME	Q9nba1 drosophila
308	217.5	12.0	1759	2	Q7PPH8_ANOGA	Q7pph8 anopheles g	381	206	11.4	1055	2	Q61YV0_CAEER	Q61yv0 caenorhabdi
309	217	12.0	885	2	Q8HYV1_PIG	Q8hyv1 sus scrofa	382	206	11.4	1187	2	Q8WR45_CAEEL	Q8wr45 caenorhabdi
310	217	12.0	886	2	Q8HYV2_PIG	Q8hyv2 sus scrofa	383	205.5	11.4	1028	1	CNTN3_RAT	Q62662 rattus norv
311	217	12.0	1443	2	Q8MTB2_DROME	Q8mtb2 drosophila	384	205.5	11.4	2016	2	Q8MKM6_DROME	Q8mkm6 drosophila
312	217	12.0	1765	2	Q9VS30_DROME	Q9vs30 drosophila	385	205.5	11.4	2016	2	Q8MKM7_DROME	Q8mkm7 drosophila
313	217	12.0	1770	2	Q9VS29_DROME	Q9vs29 drosophila	386	205.5	11.4	2019	2	Q8MKM8_DROME	Q8mkm8 drosophila
314	216.5	12.0	1048	2	Q7QH01_ANOGA	Q7qh01 anopheles g	387	205.5	11.4	17352	2	Q95YM2_PROCL	Q95ym2 procamburus
315	216.5	12.0	1109	2	Q6P5H3_MOUSE	Q6p5h3 mus musculu	388	205	11.4	432	2	Q9UJPI_HUMAN	Q9ujpi homo sapien
316	216.5	12.0	1937	2	Q7QGT8_ANOGA	Q7qgt8 anopheles g	389	204.5	11.3	439	2	O57349_CHICK	O57349 gallus gall
317	216	12.0	435	2	Q5FWM6_XENLA	Q5fwm6 xenopus lae	390	204.5	11.3	1154	2	Q4SR22_TETNG	Q4sr22 tetraodon n
318	215.5	11.9	886	2	Q9VM64_DROME	Q9vm64 drosophila	391	204.5	11.3	1377	1	NEO1_RAT	P97603 rattus norv
319	215.5	11.9	1302	1	NRG_DROME	P20241 drosophila	392	204.5	11.3	1675	2	Q98SW4_BRARE	Q98sw4 brachydanio
320	215.5	11.9	2597	2	Q6WRH9_RAT	Q6wrh9 rattus norv	393	204.5	11.3	3248	2	Q4SM90_TETNG	Q4sm90 tetraodon n
321	215	11.9	443	2	Q8WR43_CAEEL	Q8wr43 caenorhabdi	394	204.5	11.3	4129	2	Q59B65_DROME	Q59b65 drosophila
322	215	11.9	444	2	Q8MPU9_CAEEL	Q8mpu9 caenorhabdi	395	204	11.3	335	2	O5XKA0_XENLA	O5xka0 xenopus lae
323	215	11.9	904	2	Q7PWE2_ANOGA	Q7pwe2 anopheles g	396	204	11.3	437	2	Q7QG58_ANOGA	Q7qg58 anopheles g

397	204	11.3	478	2	Q4RVM0_TETNG	Q4rvm0 tetraodon n	470	198	11.0	847	1	CD22_HUMAN	P20273 homo sapien
398	204	11.3	779	2	Q4STG7_TETNG	Q4stg7 tetraodon n	471	198	11.0	907	2	Q9NEG0_DROME	Q9neg0 drosophila
399	204	11.3	1000	2	Q4TBR4_TETNG	Q4tbr4 tetraodon n	472	198	11.0	1240	1	Q4SMB8_TETNG	P97685 rattus norv
400	204	11.3	1443	1	NEO1_CHICK	Q90610 gallus gall	473	198	11.0	2007	2	Q4SM88_TETNG	Q4sm88 tetraodon n
401	203.5	11.3	978	2	Q5TVT0_BRARE	Q5tv0 brachydanio	474	198	11.0	2024	2	Q53CM6_BRARE	Q53cm6 brachydanio
402	203.5	11.3	1195	2	Q5TUS2_ANOGA	Q5tus2 anopheles g	475	197.5	10.9	1164	2	Q6MNS5_DROVI	Q6mns5 drosophila
403	203.5	11.3	1228	2	Q7QBI6_ANOGA	Q7qbi6 anopheles g	476	197.5	10.9	1228	2	Q8WRA3_DROME	Q8wra3 drosophila
404	203.5	11.3	1249	2	Q90Z04_XENILA	Q90z04 xenopus lae	477	197.5	10.9	1235	2	Q9V787_DROME	Q9v787 drosophila
405	203.5	11.3	1285	2	Q5YTT1_BRARE	Q5ytt1 brachydanio	478	197.5	10.9	1235	2	Q86BD5_DROME	Q86bd5 drosophila
406	203.5	11.3	2053	1	DSL11_HUMAN	Q8t884 homo sapien	479	197.5	10.9	1240	1	Q4SMB8_TETNG	Q4sm88 tetraodon n
407	203.5	11.3	2646	2	Q4SLN8_TETNG	Q4sln8 tetraodon n	480	197.5	10.9	1251	1	Q6ZQ54_MOUSE	Q6zq54 mus musculus
408	203	11.2	912	2	Q7SX76_BRARE	Q7sx76 brachydanio	481	197.5	10.9	1447	1	DC2_HUMAN	P43146 homo sapien
409	203	11.2	912	2	Q4SG4_TETNG	Q4sg4 tetraodon n	482	197.5	10.9	16215	2	Q9NFS3_DROME	Q9nfs3 drosophila
410	203	11.2	1006	2	Q6IDE9_DROME	Q6ide9 drosophila	483	197.5	10.9	18074	2	Q91704_DROME	Q91704 drosophila
411	203	11.2	1415	2	Q94155_CABEL	Q94155 caenorhabdi	484	197	10.9	1268	2	Q619L9_CABBR	Q61919 caenorhabdi
412	203	11.2	1950	2	Q80YN8_MOUSE	Q80yn8 mus musculus	485	196.5	10.9	1180	2	Q5IS40_PANTR	Q5is40 pan troglod
413	202.5	11.2	496	2	Q7Z075_CABEL	Q7z075 caenorhabdi	486	196.5	10.9	1301	2	Q4RSG5_TETNG	Q4rsg5 tetraodon n
414	202.5	11.2	941	2	Q4SMD8_TETNG	Q4smd8 tetraodon n	487	196	10.9	306	2	Q5H2T7_XENTR	Q5h2t7 xenopus tro
415	202.5	11.2	1066	2	Q8WRS5_DROME	Q8wrs5 drosophila	488	196	10.9	836	2	Q5W9P8_HUMAN	Q5w9f8 homo sapien
416	202.5	11.2	1946	2	Q68J72_APIME	Q68j72 apis mellif	489	196	10.9	1040	2	Q5T2F0_HUMAN	Q5t2f0 homo sapien
417	202.5	11.2	2828	2	Q9NR99_HUMAN	Q9nr99 homo sapien	490	196	10.9	1157	2	Q5T2F2_HUMAN	Q5t2f2 homo sapien
418	202	11.2	947	1	MUSK_CHICK	Q8axy6 gallus gall	491	196	10.9	1240	1	Q4SMB8_TETNG	Q4sm88 tetraodon n
419	202	11.2	1269	2	Q01632_CABEL	Q01632 caenorhabdi	492	196	10.9	1240	2	Q5T2F4_HUMAN	Q5t2f4 homo sapien
420	202	11.2	1273	2	Q4A928_CABEL	Q4a928 caenorhabdi	493	196	10.9	1347	2	Q5T2F3_HUMAN	Q5t2f3 homo sapien
421	202	11.2	1409	2	Q801M2_BRARE	Q801m2 brachydanio	494	196	10.9	1906	1	MYLK_CHICK	P11799 gallus gall
422	202	11.2	1409	2	Q8J127_BRARE	Q8j127 brachydanio	495	195.5	10.8	477	2	Q5EAJ2_FUGRU	Q5eaj2 fugu rubrip
423	202	11.2	1428	2	Q8AY67_BRARE	Q8ay67 brachydanio	496	195.5	10.8	619	2	Q5T2F6_HUMAN	Q5t2f6 homo sapien
424	202	11.2	2022	2	Q7KQ05_DROME	Q7kq05 drosophila	497	195.5	10.8	1270	2	Q9U3P2_CABEL	Q9u3p2 caenorhabdi
425	201.5	11.2	232	2	Q7Q807_ANOGA	Q7q807 anopheles g	498	195	10.8	489	2	Q4RM24_TETNG	Q4rm24 tetraodon n
426	201.5	11.2	388	2	Q8NF28_HUMAN	Q8nf28 homo sapien	499	195	10.8	1369	1	Q4SMB8_TETNG	Q4sm88 tetraodon n
427	201.5	11.2	537	2	Q7QBY8_ANOGA	Q7qby8 anopheles g	500	195	10.8	1375	2	Q8ML47_DROME	Q8ml47 drosophila
428	201.5	11.2	786	2	Q4SR20_TETNG	Q4sr20 tetraodon n	501	195	10.8	1375	2	Q94537_DROME	Q94537 drosophila
429	201.5	11.2	979	2	Q4TBU1_TETNG	Q4tbu1 tetraodon n	502	195	10.8	1386	1	ROBO3_HUMAN	Q9ems0 homo sapien
430	201.5	11.2	2008	2	Q7KSE9_DROME	Q7kse9 drosophila	503	195	10.8	1526	2	Q94538_DROME	Q94538 drosophila
431	201.5	11.2	2046	2	Q7KSE9_DROME	Q7kse9 drosophila	504	195	10.8	1526	2	Q94538_DROME	Q94538 drosophila
432	201.5	11.2	3215	2	Q8IRV7_DROME	Q8irv7 drosophila	505	194.5	10.8	1277	1	L1CAM_FUGRU	Q9wz7 fugu rubrip
433	201.5	11.2	3262	2	Q8EQJ5_MOUSE	Q8eqj5 mus musculus	506	194	10.7	949	2	Q9VWZ7_DROME	Q9vwz7 drosophila
434	201.5	11.2	4117	2	Q8IRV9_DROME	Q8irv9 drosophila	507	194	10.7	2095	2	Q4SMB8_TETNG	Q4sm88 tetraodon n
435	201.5	11.2	4179	2	Q9W4Y4_DROME	Q9w4y4 drosophila	508	193.5	10.7	1256	1	NRCAM_DROME	Q810u4 mus musculus
436	201.5	11.2	4223	2	Q8MPN3_DROME	Q8mpn3 drosophila	509	193	10.7	749	2	Q967D9_DROME	Q967d9 drosophila
437	201.5	11.2	4228	2	Q8IRV8_DROME	Q8irv8 drosophila	510	193	10.7	775	2	Q6PF50_XENILA	Q6pf50 xenopus lae
438	201.5	11.2	8647	2	Q7KQP5_DROME	Q7kqp5 drosophila	511	193	10.7	803	2	Q80ZF5_RAT	Q80zf5 rattus norv
439	201.5	11.2	8930	2	Q7KQP7_DROME	Q7kqp7 drosophila	512	193	10.7	902	2	Q81Q17_DROME	Q81q17 drosophila
440	201.5	11.2	8943	2	Q9V4F7_DROME	Q9v4f7 drosophila	513	193	10.7	903	2	Q9VQY1_DROME	Q9vy1 drosophila
441	201	11.1	487	1	FGRL1_CHICK	Q7t2h2 gallus gall	514	193	10.7	903	2	Q967D8_DROME	Q967d8 drosophila
442	201	11.1	623	2	Q8BY18_MOUSE	Q8by18 mus musculus	515	193	10.7	949	2	Q8IGN3_DROME	Q8ign3 drosophila
443	201	11.1	688	2	Q80ZE3_MOUSE	Q80ze3 mus musculus	516	193	10.7	1166	2	Q9QVN4_9MURI	Q9qvn4 rattus sp.
444	201	11.1	700	1	KIR2_MOUSE	Q7tau7 mus musculus	517	193	10.7	1508	2	Q6NR34_DROME	Q6nr34 drosophila
445	201	11.1	946	2	Q07153_TORCA	Q07153 torpedo cal	518	193	10.7	1508	2	Q9VQY2_DROME	Q9vqy2 drosophila
446	201	11.1	1296	2	Q7QJ29_ANOGA	Q7qj29 anopheles g	519	193	10.7	1531	2	Q967D7_DROME	Q967d7 drosophila
447	201	11.1	1709	1	SN_HUMAN	Q9bz22 homo sapien	520	193	10.7	2029	1	LAR_DROME	P16821 drosophila
448	200.5	11.1	1048	2	Q7QH02_ANOGA	Q7qh02 anopheles g	521	192.5	10.7	2200	2	Q4RRS2_TETNG	Q4rrs2 tetraodon n
449	200.5	11.1	1271	2	Q6U714_BRARE	Q6u714 brachydanio	522	192.5	10.7	776	2	Q4RHT1_TETNG	Q4rht1 tetraodon n
450	200.5	11.1	1447	1	DC2_MOUSE	Q70211 mus musculus	523	192.5	10.7	1150	2	Q8BS24_MOUSE	Q8bs24 mus musculus
451	200.5	11.1	1493	1	NEO1_MOUSE	Q97798 mus musculus	524	192.5	10.7	1209	2	P70232_MOUSE	P70232 mus musculus
452	200.5	11.1	5516	2	Q7Z248_BRARE	Q7z248 brachydanio	525	192.5	10.7	1259	2	Q6PGJ3_MOUSE	Q6pgj3 mus musculus
453	200	11.1	524	2	Q7PSJ8_ANOGA	Q7psj8 anopheles g	526	192.5	10.7	1260	1	L1CAM_MOUSE	P11827 mus musculus
454	200	11.1	1253	2	Q4SCT8_TETNG	Q4sct8 tetraodon n	527	192.5	10.7	1284	1	NRCAM_CHICK	P35331 gallus gall
455	199.5	11.0	1031	2	Q597F7_BRARE	Q597f7 brachydanio	528	192	10.6	211	2	Q7PVK5_ANOGA	Q7pvk5 anopheles g
456	199.5	11.0	1209	2	Q7PG72_ANOGA	Q7pg72 anopheles g	529	192	10.6	399	2	Q8N772_HUMAN	Q8n772 homo sapien
457	199.5	11.0	1245	2	Q7QEC1_ANOGA	Q7qec1 anopheles g	530	192	10.6	529	1	FGRL1_MOUSE	Q81v87 mus musculus
458	199.5	11.0	1465	2	Q63155_RAT	Q63155 rattus norv	531	192	10.6	602	2	Q86YJ5_HUMAN	Q86yj5 homo sapien
459	199.5	11.0	1465	2	Q7TQG5_MOUSE	Q7tqg5 mus musculus	532	192	10.6	606	2	Q8NA84_HUMAN	Q8na84 homo sapien
460	199	11.0	165	2	Q7Q8F3_ANOGA	Q7q8f3 anopheles g	533	192	10.6	650	2	Q8NA84_HUMAN	Q8na84 homo sapien
461	199	11.0	440	2	Q6ZMD4_HUMAN	Q6zmd4 homo sapien	534	192	10.6	771	2	Q4RMQ7_HUMAN	Q4rmq7 homo sapien
462	199	11.0	529	2	Q4SMH3_TETNG	Q4smh3 tetraodon n	535	192	10.6	1256	2	Q35158_RAT	Q35158 rattus norv
463	199	11.0	940	2	Q8NFA7_HUMAN	Q8nfa7 homo sapien	536	192	10.6	1304	1	NRCAM_HUMAN	Q92823 homo sapien
464	199	11.0	1241	1	NPN_HUMAN	Q60500 homo sapien	537	192	10.6	1378	1	ROBO2_HUMAN	Q9hck4 homo sapien
465	199	11.0	1513	2	Q90Z70_BRARE	Q90z70 brachydanio	538	191.5	10.6	1060	2	Q9QZ13_RAT	Q9qz13 rattus norv
466	199	11.0	1723	2	Q8CHB2_MOUSE	Q8chb2 mus musculus	539	191	10.6	1239	2	Q41PF2_CABBR	Q41pf2 caenorhabdi
467	198.5	11.0	931	2	Q6KAM5_MOUSE	Q6kam5 mus musculus	540	191	10.6	2154	2	Q8WZ51_HUMAN	Q8wz51 homo sapien
468	198	11.0	437	2	Q86YV1_HUMAN	Q86yv1 homo sapien	541	190.5	10.5	388	2	Q8R464_MOUSE	Q8r464 mus musculus
469	198	11.0	662	2	Q60926_HUMAN	Q60926 homo sapien	542	190.5	10.5	1154	2	Q9QVN3_9MURI	Q9qvn3 rattus sp.

543	190.5	10.5	1194	2	Q6PW35_RAT	Q6pw35	rattus norv
544	190.5	10.5	1197	2	Q6PW38_RAT	Q6pw38	rattus norv
545	190.5	10.5	1198	2	Q6PW37_RAT	Q6pw37	rattus norv
546	190.5	10.5	1206	2	Q6PW36_RAT	Q6pw36	rattus norv
547	190.5	10.5	1209	2	Q6PW39_RAT	Q6pw39	rattus norv
548	190.5	10.5	1214	1	NRCAM_RAT	P97686	rattus norv
549	190.5	10.5	1239	2	Q6PW34_RAT	Q6pw34	rattus norv
550	190.5	10.5	1366	1	ROBQ3_MOUSE	Q92214	mus musculus
551	190.5	10.5	4001	2	Q9N2P7_DROME	Q9n2p7	drosophila
552	190.5	10.5	4796	2	Q9N188_DROME	Q9n188	drosophila
553	190.5	10.5	4796	2	Q9W055_DROME	Q9w055	drosophila
554	190	10.5	345	2	Q811H7_MOUSE	Q811h7	mus musculus
555	190	10.5	381	2	Q9Y4A4_HUMAN	Q9y4a4	homo sapien
556	190	10.5	551	2	Q8NH7_HUMAN	Q8nh7	homo sapien
557	190	10.5	619	2	Q7PX10_ANOGA	Q7px10	anopheles g
558	190	10.5	1077	2	Q5WN88_CAER	Q5wn88	caenorhabdi
559	190	10.5	1090	2	Q4TAD5_TETNG	Q4tad5	tetraodon n
560	190	10.5	1406	2	Q9GPP7_DROME	Q9gpp7	drosophila
561	190	10.5	1463	2	Q9VQ08_DROME	Q9vq08	drosophila
562	189.5	10.5	433	2	Q9V644_DROME	Q9v644	drosophila
563	189.5	10.5	602	2	Q9VFD9_DROME	Q9vfd9	drosophila
564	189.5	10.5	765	2	Q9TWA4_APLCA	Q9twa4	aplysia cal
565	189.5	10.5	765	2	Q9BKQ1_APLCA	Q9bkq1	aplysia cal
566	189.5	10.5	812	2	Q9BKQ0_APLCA	Q9bkq0	aplysia cal
567	189.5	10.5	812	2	Q9TWA5_APLCA	Q9twa5	aplysia cal
568	189.5	10.5	880	2	Q7KPQ8_DROME	Q7kpq8	drosophila
569	189.5	10.5	932	2	Q9TWA6_APLCA	Q9twa6	aplysia cal
570	189.5	10.5	932	2	Q9BKP9_APLCA	Q9bkp9	aplysia cal
571	189.5	10.5	1180	2	Q51S85_9PRIM	Q51s85	gallmri bol
572	189.5	10.5	1280	2	Q9O933_CHICK	Q9o933	gallus gall
573	189	10.5	595	2	Q7Q3K8_ANOGA	Q7q3k8	anopheles g
574	189	10.5	750	2	Q646H5_CAEL	Q646h5	caenorhabdi
575	189	10.5	1238	2	Q58QC3_XENLA	Q58qc3	xenopus lae
576	189	10.5	1288	2	Q624K5_CAER	Q624k5	caenorhabdi
577	189	10.5	1340	2	Q5U176_DROME	Q5u176	drosophila
578	188.5	10.4	418	2	Q5O1T5_BRARE	Q5o1t5	brachydanio
579	188.5	10.4	1032	1	CNTIA_BRARE	Q8axx4	brachydanio
580	188.5	10.4	1328	2	Q589G5_CHICK	Q589g5	gallus gall
581	188.5	10.4	1328	2	Q4RKW3_TETNG	Q4rkw3	tetraodon n
582	188.5	10.4	1390	1	CONT_DROME	Q9vnl4	drosophila
583	188.5	10.4	1390	2	Q5B191_DROME	Q5b191	drosophila
584	188.5	10.4	2343	2	Q5TX11_ANOGA	Q5tx11	anopheles g
585	188	10.4	325	2	Q4SXS1_TETNG	Q4sxs1	tetraodon n
586	188	10.4	495	2	Q4TAJ7_TETNG	Q4taj7	tetraodon n
587	188	10.4	529	1	FGRL1_RAT	Q7tgm3	rattus norv
588	188	10.4	529	1	Q4V8P8_RAT	Q4v8p8	rattus norv
589	188	10.4	789	1	KIRRI_MOUSE	Q8QW68	mus musculus
590	188	10.4	1177	2	Q6GQB1_XENLA	Q6gqb1	xenopus lae
591	187.5	10.4	434	2	Q4RRG0_TETNG	Q4rrg0	tetraodon n
592	187.5	10.4	538	2	Q9YQ07_MOUSE	Q9yq07	mus musculus
593	187.5	10.4	893	2	Q5TWT4_ANOGA	Q5twt4	anopheles g
594	187.5	10.4	1250	2	Q88971_MOUSE	Q88971	mus musculus
595	187.5	10.4	1259	1	L1CAM_RAT	Q88971	mus musculus
596	187.5	10.4	1266	1	NGCA_CHICK	Q05695	rattus norv
597	187.5	10.4	2419	2	Q7PXZ1_ANOGA	Q03696	gallus gall
598	187	10.4	687	2	Q7ZTN4_XENLA	Q7pxz1	anopheles g
599	187	10.4	778	1	KIRK3_HUMAN	Q7ztm4	xenopus lae
600	187	10.4	888	2	Q4VBK2_BRARE	Q81zu3	homo sapien
601	187	10.4	1470	1	ROBO2_MOUSE	Q4vbk2	brachydanio
602	187	10.4	2174	2	Q9GQ07_DROME	Q7tpd3	mus musculus
603	187	10.4	2995	2	Q696W0_BRARE	Q9gq07	drosophila
604	187	10.4	4071	2	Q7PH68_ANOGA	Q696w0	brachydanio
605	187	10.4	4098	2	Q7PQG9_ANOGA	Q7ph68	anopheles g
606	186.5	10.3	922	2	Q9O413_BRARE	Q7pqs9	anopheles g
607	186.5	10.3	1150	2	Q4SL82_TETNG	Q9O413	brachydanio
608	186.5	10.3	1264	2	Q14631_HUMAN	Q4sl82	tetraodon n
609	186.5	10.3	1725	2	Q7Q916_ANOGA	Q14631	homo sapien
610	186.5	10.3	1879	2	Q7Q0X2_ANOGA	Q7q916	anopheles g
611	186.5	10.3	1944	2	Q4SPG3_TETNG	Q7q0x2	anopheles g
612	186.5	10.3	1995	2	Q5TNW7_ANOGA	Q4spg3	tetraodon n
613	186	10.3	708	1	KIRR2_HUMAN	Q5tnw7	anopheles g
614	186	10.3	882	2	Q4RVZ3_TETNG	O6tw16	homo sapien
615	186	10.3	1225	2	Q6GP61_XENLA	Q4rvz3	tetraodon n

Q6nr91	drosophila
Q7kqp6	drosophila
Q86sn1	homo sapien
Q15109	homo sapien
P06731	caenorhabdi
Q84h40	homo sapien
Q48h6	tetraodon n
Q8mmj9	bombyx mori
Q8t101	bombyx mori
Q7pvm1	anopheles g
Q501u7	brachydanio
Q8r4b5	mus musculus
Q8br86	mus musculus
Q6x936	rattus norv
Q8nhn0	homo sapien
Q8w552	homo sapien
Q91562	xenopus lae
Q8c6w0	mus musculus
Q6gmz9	xenopus lae
Q53g30	homo sapien
Q695l1	homo sapien
P07722	rattus norv
Q53hd1	homo sapien
Q963h4	homo sapien
Q5w0f8	homo sapien
Q9v643	drosophila
Q24327	drosophila
Q8axb3	brachydanio
Q4kng0	homo sapien
Q725n4	homo sapien
Q4t444	tetraodon n
Q4t680	tetraodon n
Q5esn1	bos taurus
Q5jlr9	brachydanio
Q90284	caerassius a
Q21043	caenorhabdi
Q8t103	bombyx mori
Q9xxd7	caenorhabdi
Q5j2p6	homo sapien
Q8nt26	homo sapien
Q44087	caenorhabdi
Q76698	caenorhabdi
Q961d6	drosophila
Q9bn17	drosophila
Q9vqW7	drosophila
P53767	rattus norv
Q695l3	brachydanio
Q56784	homo sapien
P20916	homo sapien
Q53es7	homo sapien
Q59gd9	homo sapien
Q9g6h3	halocynthia
Q8nhn3	homo sapien
Q4sln7	tetraodon n
Q7rtl4	drosophila
Q5rjw1	mus musculus
Q8bq3	mus musculus
Q90478	brachydanio
P35969	mus musculus
Q5w0f9	homo sapien
Q4sif9	tetraodon n
Q8n237	homo sapien
Q8t3es	caenorhabdi
Q19128	caenorhabdi
Q8m986	caenorhabdi
Q69vj3	homo sapien
Q723b7	homo sapien
Q9u898	manduca sex
Q4z220	homo sapien
Q8w553	homo sapien
Q25198	hydra atten
Q9qz87	mus musculus

689	180.5	10.0	1256	2	Q925S5_MOUSE	Q925s5 mus musculus	762	174.5	9.7	1792	2	Q4SK53_TETNG	Q4sk53 tetraodon n
690	180.5	10.0	1256	2	Q9JIX1_MOUSE	Q9jix1 mus musculus	763	174	9.6	452	2	Q4R5Y9_MACEA	Q4r5y9 macaca faec
691	180.5	10.0	1256	2	Q9ET59_MOUSE	Q9et59 mus musculus	764	174	9.6	534	2	Q866T2_PANTR	Q866t2 pan troglod
692	180.5	10.0	1269	2	Q6U715_BRARE	Q6u715 brachydanio	765	174	9.6	626	2	Q53HA1_HUMAN	Q53ha1 homo sapien
693	180.5	10.0	1534	2	Q4RRJ4_TETNG	Q4rrj4 tetraodon n	766	174	9.6	630	2	Q7QBL9_ANOGA	Q7qbl9 anopheles g
694	180	10.0	413	2	Q27418_MNSE	Q27418 manduca sex	767	174	9.6	675	2	Q7T0V5_XENLA	Q7t0v5 xenopus lae
695	180	10.0	571	2	Q5W0G0_HUMAN	Q5w0g0 homo sapien	768	174	9.6	736	2	Q8MYS2_DROME	Q8mys2 drosophila
696	180	10.0	606	2	Q7QHA0_ANOGA	Q7qha0 anopheles g	769	174	9.6	774	2	Q9V930_DROME	Q9v930 drosophila
697	180	10.0	626	2	Q5R4C0_PONPY	Q5r4c0 pongo pygma	770	174	9.6	1255	2	Q7YQL7_PONPY	Q7yql7 pongo pygma
698	180	10.0	1335	2	Q610C7_CAEBR	Q610c7 caenorhabdi	771	174	9.6	1255	2	Q7YQL8_PANTR	Q7yql8 pan troglod
699	180	10.0	18412	2	Q7Z261_BRARE	Q7z261 brachydanio	772	174	9.6	1721	2	Q961U1_DROME	Q961u1 drosophila
700	179.5	9.9	333	2	Q90241_CHICK	Q90241 gallus gall	773	174	9.6	1748	2	Q4S3Q6_TETNG	Q4s3q6 tetraodon n
701	179.5	9.9	362	2	Q9JHQ1_RAT	Q9jhq1 rattus norv	774	174	9.6	2389	2	Q6BEQ6_CAEBL	Q6beq6 caenorhabdi
702	179.5	9.9	503	2	Q9W259_DROME	Q9w259 drosophila	775	174	9.6	3375	1	UNC52_CAEBL	Q05561 caenorhabdi
703	179.5	9.9	735	2	Q4RZE9_TETNG	Q4rze9 tetraodon n	776	174	9.6	4650	2	Q15598_HUMAN	Q15598 homo sapien
704	179.5	9.9	804	2	Q800Z1_BRARE	Q800z1 brachydanio	777	174	9.6	6658	2	Q76281_DROME	Q76281 drosophila
705	179.5	9.9	806	2	Q90Z00_BRARE	Q90z00 brachydanio	778	173.5	9.6	360	2	Q8MRE6_DROME	Q8mre6 drosophila
706	179	9.9	300	1	JAM1_MOUSE	Q88792 mus musculus	779	173.5	9.6	442	2	Q6KAT6_MOUSE	Q6kat6 mus musculus
707	179	9.9	300	2	Q8VC39_MOUSE	Q8vc39 mus musculus	780	173.5	9.6	463	2	Q7PN36_ANOGA	Q7pn36 anopheles g
708	179	9.9	626	1	MAG_MOUSE	P20917 mus musculus	781	173.5	9.6	525	2	Q5R9N6_PONPY	Q5r9n6 pongo pygma
709	179	9.9	782	2	Q4SI43_TETNG	Q4si43 tetraodon n	782	173.5	9.6	538	2	Q9NMQ7_HUMAN	Q9nqw7 homo sapien
710	179	9.9	814	1	PUNC_HUMAN	Q81vul homo sapien	783	173.5	9.6	766	2	Q7Q0S7_ANOGA	Q7q0s7 anopheles g
711	179	9.9	917	1	ICAM5_MOUSE	Q60625 mus musculus	784	173.5	9.6	1021	2	P79757_CHICK	P79757 gallus gall
712	179	9.9	1019	2	Q8BJK6_MOUSE	Q8bjk6 mus musculus	785	173.5	9.6	4463	2	Q8MLD8_DROME	Q8mld8 drosophila
713	179	9.9	3117	2	Q7QJK9_ANOGA	Q7qjk9 anopheles g	786	173.5	9.6	9270	2	Q8MLD9_DROME	Q8mld9 drosophila
714	178.5	9.9	603	2	Q4SLP0_TETNG	Q4slp0 tetraodon n	787	173	9.6	385	2	Q9UQF5_HUMAN	Q9uqf5 homo sapien
715	178.5	9.9	1234	1	NPHN_RAT	Q9r044 rattus norv	788	173	9.6	410	2	Q6R3M0_BOMMO	Q6r3m0 bombyx mori
716	178.5	9.9	1252	2	Q9JIX2_RAT	Q9jix2 rattus norv	789	173	9.6	410	2	Q6R3M2_BOMMO	Q6r3m2 bombyx mori
717	178.5	9.9	2293	2	Q4T1M4_TETNG	Q4t1m4 tetraodon n	790	173	9.6	410	2	Q7YZA7_BOMMO	Q7yza7 bombyx mori
718	178	9.9	379	2	Q9CWM1_MOUSE	Q9cwm1 mus musculus	791	173	9.6	1248	2	Q9XT41_CERAE	Q9xt41 cercopitheci
719	178	9.9	413	1	HEMO_MNSE	P31398 manduca sex	792	172.5	9.6	357	2	Q8R112_MOUSE	Q8r112 mus musculus
720	178	9.9	492	2	Q9ET54_MOUSE	Q9et54 mus musculus	793	172.5	9.6	1880	2	O18465_HIRME	O18465 hirtudo medi
721	178	9.9	563	2	Q5FWR8_XENTR	Q5fwr8 xenopus tro	794	172	9.5	287	2	Q13984_HUMAN	Q13984 homo sapien
722	178	9.9	853	2	Q6DFX7_MOUSE	Q6dfx7 mus musculus	795	172	9.5	319	1	GPA33_MOUSE	Q91ka37 homo sapien
723	178	9.9	1073	2	Q9TXI8_CAEBL	Q9txi8 caenorhabdi	796	172	9.5	1045	2	Q86T37_HUMAN	Q86t37 homo sapien
724	178	9.9	1081	2	Q692T7_MOUSE	Q692t7 mus musculus	797	172	9.5	1045	2	Q5VV36_HUMAN	Q5vv36 homo sapien
725	178	9.9	1400	2	Q7PE94_ANOGA	Q7pe94 anopheles g	798	172	9.5	1320	2	Q96KF5_HUMAN	Q96kf5 homo sapien
726	177.5	9.8	344	2	Q9VY33_DROME	Q9vy33 drosophila	799	172	9.5	1320	2	Q86TC9_HUMAN	Q86tc9 homo sapien
727	177.5	9.8	457	2	Q960D1_DROME	Q960d1 drosophila	800	172	9.5	1403	2	Q5VV35_HUMAN	Q5vv35 homo sapien
728	177.5	9.8	583	1	CD166_BOVIN	Q9bh13 bos taurus	801	172	9.5	2403	2	Q8MLD5_DROME	Q8mld5 drosophila
729	177.5	9.8	717	2	Q7PQI1_ANOGA	Q7pqul anopheles g	802	172	9.5	4736	2	Q7YT99_MITGA	Q7yt99 mytilus gal
730	177.5	9.8	796	2	Q91287_PLEWA	Q91287 pleurodeles	803	172	9.5	7210	2	Q9V7G8_DROME	Q9v7g8 drosophila
731	177.5	9.8	1249	2	Q7TMZ9_RAT	Q7tmz9 rattus norv	804	171.5	9.5	283	2	Q9VT76_DROME	Q9vt76 drosophila
732	177.5	9.8	1527	2	Q9VZZ4_DROME	Q9vzz4 drosophila	805	171.5	9.5	307	2	Q94431_CICIN	Q94431 ciona intes
733	177.5	9.8	1933	2	Q6V3A4_MOUSE	Q6v3a4 mus musculus	806	171.5	9.5	1338	1	VGFRI_HUMAN	P17948 h vasculat
734	177	9.8	376	2	Q90Z71_BRARE	Q90z71 brachydanio	807	171.5	9.5	2772	2	Q9VAV4_DROME	Q9vav4 drosophila
735	177	9.8	404	2	Q9Y3E9_HUMAN	Q9y3e9 homo sapien	808	171.5	9.5	2894	2	Q7KRX2_DROME	Q7krx2 drosophila
736	177	9.8	410	2	Q4FAT1_BOMMO	Q4fat1 bombyx mori	809	171.5	9.5	26926	2	Q4U1Z6_HUMAN	Q4ulz6 homo sapien
737	177	9.8	467	2	Q4R5P0_MACFA	Q4r5p0 macaca faec	810	171	9.5	373	2	Q7KYP5_HUMAN	Q7kyp5 homo sapien
738	177	9.8	474	2	Q5FV48_FUGRU	Q5fv48 fugu rubrip	811	171	9.5	464	2	Q16170_HUMAN	Q16170 homo sapien
739	177	9.8	577	2	Q80Y42_MOUSE	Q80y42 mus musculus	812	171	9.5	468	2	Q96CA7_HUMAN	Q96ca7 homo sapien
740	177	9.8	1001	2	Q5TR64_ANOGA	Q5tr64 anopheles g	813	171	9.5	526	1	CEAMI_HUMAN	P13688 homo sapien
741	177	9.8	2242	2	Q9P2P9_HUMAN	Q9p2p9 homo sapien	814	171	9.5	534	2	Q86SE4_HUMAN	Q86se4 homo sapien
742	177	9.8	8625	2	Q86GD6_PROCL	Q86gd6 procambur	815	171	9.5	764	2	Q8MQO1_DROME	Q8mqo1 drosophila
743	176.5	9.8	510	2	Q7L3E0_HUMAN	Q7l3e0 homo sapien	816	171	9.5	810	2	Q9PS96_XENLA	Q9ps96 xenopus lae
744	176.5	9.8	586	1	SIG11_HUMAN	Q96x16 homo sapien	817	171	9.5	937	2	Q5WN68_CAEBR	Q5wn68 caenorhabdi
745	176.5	9.8	772	2	Q9Y2J6_HUMAN	Q9y2j6 homo sapien	818	171	9.5	1255	2	Q7Z329_HUMAN	Q7z329 homo sapien
746	176.5	9.8	1106	2	Q8WX93_HUMAN	Q8wx93 homo sapien	819	171	9.5	1257	1	LICAM_HUMAN	P32004 homo sapien
747	176.5	9.8	2169	2	Q8AV58_CHICK	Q8av58 gallus gall	820	171	9.5	2016	2	Q86BQ7_DROME	Q86bq7 drosophila
748	176.5	9.8	3165	2	Q7Q767_ANOGA	Q7q767 anopheles g	821	171	9.5	2224	2	Q9U1M1_DROME	Q9u1m1 drosophila
749	176	9.1	410	2	Q6R3L9_BOMMA	Q6r3l9 bombyx mand	822	171	9.5	26926	2	Q8WZB3_HUMAN	Q8wzb3 homo sapien
750	176	9.7	416	2	Q7Q1Z7_ANOGA	Q7q1z7 anopheles g	823	170.5	9.4	370	2	Q800Y8_BRARE	Q800y8 brachydanio
751	176	9.7	577	2	Q9D2Z1_MOUSE	Q9d2z1 m mus muscu	824	170.5	9.4	501	2	Q6Q147_BOVIN	Q6q147 bos taurus
752	176	9.7	964	2	Q18382_CAEBL	Q18382 caenorhabdi	825	170.5	9.4	521	1	CD166_RABIT	Q04651 corytolagus
753	176	9.7	1319	2	Q4T8B2_TETNG	Q4t8b2 tetraodon n	826	170.5	9.4	540	2	Q8N0Z9_HUMAN	Q8n0z9 homo sapien
754	175.5	9.7	1196	2	Q65Z10_CAEBL	Q65z10 caenorhabdi	827	170.5	9.4	591	2	Q6NP04_DROME	Q6np04 drosophila
755	175.5	9.7	1227	2	Q9BIA2_CAEBL	Q9bia2 caenorhabdi	828	170.5	9.4	1197	2	Q4RVM1_TETNG	Q4rvml tetraodon n
756	175.5	9.7	1505	2	Q7Q623_ANOGA	Q7q623 anopheles g	829	170	9.4	255	2	Q60YE7_CAEBR	Q60ye7 caenorhabdi
757	175	9.7	234	2	Q81ZQ9_HUMAN	Q81zq9 homo sapien	830	170	9.4	291	2	Q66J15_XENTR	Q66j15 xenopus tro
758	175	9.7	949	2	Q4SL83_TETNG	Q4sl83 tetraodon n	831	170	9.4	300	1	JAMI_RAT	Q9j1y1 rattus norv
759	175	9.7	1391	2	Q8N3L4_HUMAN	Q8n3l4 homo sapien	832	170	9.4	486	2	Q7PSS9_ANOGA	Q7ps99 anopheles g
760	174.5	9.7	1140	2	Q4RRD1_TETNG	Q4rrd1 tetraodon n	833	170	9.4	812	1	FGFRI_XENLA	P22182 xenopus lae
761	174.5	9.7	1250	2	Q624J4_CAEBR	Q624j4 caenorhabdi	834	169.5	9.4	265	2	Q7PUU3_ANOGA	Q7puu3 anopheles g

835	169.5	9.4	351	2	Q8JFU3_BRARE	Q8jfu3 brachydanio	908	164.5	9.1	583	1	CD166_HUMAN	Q13740 homo sapien
836	169.5	9.4	351	2	Q7SY58_BRARE	Q7sy58 brachydanio	909	164.5	9.1	583	1	CD166_RAT	Q35112 rattus norv
837	169.5	9.4	402	1	RAGE_RAT	Q63495 rattus norv	910	164.5	9.1	639	2	Q96P30_HUMAN	Q96P30 homo sapien
838	169.5	9.4	402	2	Q6MG86_RAT	Q6mg86 rattus norv	911	164.5	9.1	822	2	Q61674_DROME	Q61674 drosophila
839	169.5	9.4	698	2	Q5TN75_ANOGA	Q5tn75 anopheles g	912	164.5	9.1	822	2	Q9V6T1_DROME	Q9v6t1 drosophila
840	169.5	9.4	954	2	Q7PV74_ANOGA	Q7pv74 anopheles g	913	164.5	9.1	851	2	Q7Q0S6_ANOGA	Q7q0s6 anopheles g
841	169.5	9.4	968	2	Q4W447_HORSE	Q4w447 equus caball	914	164.5	9.1	1464	2	Q4SK55_TETNG	Q4sk55 tetraodon n
842	169.5	9.4	1338	2	Q5TAR1_HUMAN	Q5tar1 homo sapien	915	164	9.1	310	1	JAM3_MOUSE	Q9d857 mus musculu
843	169.5	9.4	2200	2	Q7YRF6_CANFA	Q7yrf6 canis famil	916	164	9.1	310	1	JAM3_RAT	Q9d857 mus musculu
844	169	9.4	368	2	Q5UB49_HUMAN	Q5ub49 homo sapien	917	164	9.1	465	2	Q59E14_DROME	Q59e14 drosophila
845	169	9.4	714	2	Q4T313_TETNG	Q4t313 tetraodon n	918	164	9.1	542	2	Q5USW7_MOUSE	Q5usw7 mus musculu
846	169	9.4	764	1	ICCR_DROME	Q8l180 drosophila	919	164	9.1	628	1	LU_HUMAN	P50895 homo sapien
847	169	9.4	764	2	Q9W4U1_DROME	Q9w4u1 drosophila	920	164	9.1	812	2	Q8N612_HUMAN	Q8n612 homo sapien
848	169	9.4	814	2	Q91897_XENLA	Q91897 xenopus lae	921	164	9.1	820	2	Q8CIM9_MOUSE	Q8cim9 mus musculu
849	169	9.4	1254	2	Q674V1_PODCA	Q674v1 podocoryne	922	164	9.1	924	2	Q8TAM9_HUMAN	Q8tam9 homo sapien
850	169	9.4	1379	2	Q5XNV9_PETWA	Q5xnv9 petromyzon	923	164	9.1	998	2	Q59R27_DROME	Q59r27 drosophila
851	169	9.4	1415	2	Q5XNV8_PETWA	Q5xnv8 petromyzon	924	164	9.1	1311	2	Q961K8_DROME	Q961k8 drosophila
852	168.5	9.3	793	2	Q4RFN0_TETNG	Q4rfn0 tetraodon n	925	164	9.1	1994	2	Q6ZPP2_MOUSE	Q6zpp2 mus musculu
853	168.5	9.3	800	2	Q86LF9_DROVI	Q86lf9 drosophila	926	164	9.1	2176	2	Q6V4S5_MOUSE	Q6v4s5 mus musculu
854	168.5	9.3	801	2	Q86LF8_DROVI	Q86lf8 drosophila	927	163.5	9.1	481	2	Q5K373_BRARE	Q5k373 brachydanio
855	168.5	9.3	2159	2	Q6PAL2_MOUSE	Q6pal2 mus musculu	928	163.5	9.1	481	2	Q5K374_BRARE	Q5k374 brachydanio
856	168.5	9.3	7759	2	Q4RE90_TETNG	Q4re90 tetraodon n	929	163.5	9.1	483	2	Q9DBP8_MOUSE	Q9dbp8 mus musculu
857	168	9.3	215	2	Q9VRL5_DROME	Q9vrl5 drosophila	930	163.5	9.1	508	2	Q8CED8_MOUSE	Q8ced8 mus musculu
858	168	9.3	827	2	Q6GNS5_XENLA	Q6gns5 xenopus lae	931	163.5	9.1	508	2	Q8R0U7_MOUSE	Q8r0u7 mus musculu
859	168	9.3	1451	2	Q59EB0_HUMAN	Q59eb0 homo sapien	932	163.5	9.1	513	2	Q9D6N4_MOUSE	Q9d6n4 mus musculu
860	168	9.3	2051	2	Q44328_HIRME	Q44328 hirudo medi	933	163.5	9.1	570	2	Q5R640_PONPY	Q5r640 pongo pygma
861	167.5	9.3	555	1	CD166_CARAU	Q90304 carassius a	934	163.5	9.1	646	2	Q6PHR3_HUMAN	Q6phr3 homo sapien
862	167.5	9.3	784	2	Q81063_DROVI	Q8i063 drosophila	935	163.5	9.1	659	2	Q59E86_HUMAN	Q59e86 homo sapien
863	167.5	9.3	939	2	Q9VH85_DROME	Q9vh85 drosophila	936	163.5	9.1	1596	2	Q9HCL6_HUMAN	Q9hcl6 homo sapien
864	167.5	9.3	1019	2	Q9Y6L9_HUMAN	Q9y6l9 homo sapien	937	163	9.0	357	2	Q18872_PIG	Q18872 sus scrofa
865	167.5	9.3	1198	2	Q60T65_CAEBR	Q60t65 caenorhabdi	938	163	9.0	924	1	ICAM5_HUMAN	Q9umf0 homo sapien
866	167.5	9.3	1694	1	SN_MOUSE	Q62230 mus musculu	939	163	9.0	1357	2	Q5GIT2_BRARE	Q5git2 brachydanio
867	167.5	9.3	2776	2	Q869A0_DROME	Q869a0 drosophila	940	162.5	9.0	199	2	Q7OK35_ANOGA	Q7ok35 anopheles g
868	167.5	9.3	2898	2	Q86829_DROME	Q86829 drosophila	941	162.5	9.0	332	2	Q684Q2_MOUSE	Q684q2 mus musculu
869	167.5	9.3	5724	2	Q7PT04_ANOGA	Q7pt04 anopheles g	942	162.5	9.0	353	2	Q86X13_HUMAN	Q86xy3 homo sapien
870	167	9.2	376	2	Q9QW78_9MURI	Q9qw78 mus sp. fib	943	162.5	9.0	508	1	FCRL2_HUMAN	Q96l19 xenopus lae
871	167	9.2	551	2	Q8MSN7_DROME	Q8msn7 drosophila	944	162.5	9.0	605	2	Q6GNL9_XENLA	Q6gnl9 bos taurus
872	167	9.2	956	2	Q9W4T9_DROME	Q9w4t9 drosophila	945	162.5	9.0	628	2	Q9MZ08_BOVIN	Q9mz08 bos taurus
873	167	9.2	959	2	Q9N9Y9_DROME	Q9n9y9 drosophila	946	162.5	9.0	1509	2	Q9SP10_DROME	Q9sp10 drosophila
874	167	9.2	1276	2	Q90X22_BRARE	Q90x22 brachydanio	947	162.5	9.0	1535	2	Q23391_DROME	Q23391 drosophila
875	167	9.2	1328	2	Q4PIU9_CAEBL	Q4piu9 caenorhabdi	948	162	9.0	385	2	Q4SQV8_TETNG	Q4sqv8 tetraodon n
876	167	9.2	1331	2	Q53U87_CAEBL	Q53u87 caenorhabdi	949	162	9.0	1304	2	Q9VBES_DROME	Q9vbes drosophila
877	167	9.2	1356	1	VGFR2_HUMAN	P35968 homo sapien	950	162	9.0	4824	2	Q95YM1_PROCL	Q95ym1 procamburus
878	167	9.2	2057	2	Q4T2N4_TETNG	Q4t2n4 tetraodon n	951	161.5	8.9	197	2	Q7PTP6_ANOGA	Q7ptp6 anopheles g
879	167	9.2	2200	1	LAR_CAEBL	Q9bmn8 caenorhabdi	952	161.5	8.9	300	2	Q7PV30_ANOGA	Q7pv30 anopheles g
880	167	9.2	2295	2	Q61GU4_CAEBR	Q61gu4 caenorhabdi	953	161.5	8.9	319	2	Q7QLK4_ANOGA	Q7qlk4 anopheles g
881	166.5	9.2	1357	2	Q5GIT4_BRARE	Q5git4 brachydanio	954	161.5	8.9	350	2	Q9VFU7_DROME	Q9vfu7 drosophila
882	166.5	9.2	1506	2	Q9V7G6_DROME	Q9v7g6 drosophila	955	161.5	8.9	402	2	Q9NAR0_CAEBL	Q9nar0 caenorhabdi
883	166.5	9.2	4039	2	Q7ZZ46_BRARE	Q7zz46 brachydanio	956	161.5	8.9	650	2	Q9GKR2_BOVIN	Q9gkr2 bos taurus
884	166	9.2	407	2	Q7Q1Q0_ANOGA	Q7q1q0 anopheles g	957	161.5	8.9	739	2	Q9GKR3_BOVIN	Q9gkr3 bos taurus
885	166	9.2	576	2	Q8MYR8_DROME	Q8myr8 drosophila	958	161.5	8.9	802	2	Q42127_XENLA	Q42127 xenopus lae
886	166	9.2	590	2	Q4SPB8_TETNG	Q4spb8 tetraodon n	959	161.5	8.9	2325	2	Q9N3X8_CAEBL	Q9n3x8 caenorhabdi
887	166	9.2	591	2	Q4T2M0_TETNG	Q4t2m0 tetraodon n	960	161.5	8.9	2935	2	Q7Z1Y4_DROME	Q7z1y4 drosophila
888	166	9.2	997	2	Q7PXX0_ANOGA	Q7pxx0 anopheles g	961	161.5	8.9	2946	2	Q9W053_DROME	Q9w053 drosophila
889	166	9.2	1232	2	Q8TCG8_HUMAN	Q8tcg8 homo sapien	962	161	8.9	298	2	Q8INK5_DROME	Q8ink5 drosophila
890	165.5	9.2	340	2	Q9W3N2_DROME	Q9w3n2 drosophila	963	161	8.9	310	1	JAM3_HUMAN	Q9bxf7 homo sapien
891	165.5	9.2	538	2	Q28939_PIG	Q28939 sus scrofa	964	161	8.9	336	2	Q961T8_DROME	Q961t8 drosophila
892	165.5	9.2	543	2	Q4R603_WACFA	Q4r603 macaca fasc	965	161	8.9	461	2	Q13854_HUMAN	Q13854 homo sapien
893	165.5	9.2	646	1	MUC18_HUMAN	P43121 homo sapien	966	161	8.9	527	2	Q6ZTR2_HUMAN	Q6ztr2 homo sapien
894	165.5	9.2	1023	2	Q9ULI7_HUMAN	Q9uli7 homo sapien	967	161	8.9	538	2	Q29123_PIG	Q29123 sus scrofa
895	165.5	9.2	1193	2	Q9VQW1_DROME	Q9vqw1 drosophila	968	161	8.9	605	2	Q8TBU0_HUMAN	Q8tbu0 homo sapien
896	165.5	9.2	3158	2	Q4TAD4_TETNG	Q4tad4 tetraodon n	969	161	8.9	693	2	Q9UPU1_HUMAN	Q9upu1 homo sapien
897	165.5	9.2	4648	2	Q4T3W5_TETNG	Q4t3w5 tetraodon n	970	161	8.9	820	2	Q5R8Q3_PONPY	Q5r8q3 pongo pygma
898	165	9.1	154	2	Q7PSN2_ANOGA	Q7psn2 anopheles g	971	161	8.9	1327	2	Q8QHL3_CHICK	Q8qhl3 gallus gall
899	165	9.1	341	2	Q5TQC8_ANOGA	Q5tqc8 anopheles g	972	161	8.9	1345	2	Q8VCD0_MOUSE	Q8vcd0 mus musculu
900	165	9.1	394	2	Q52KK7_XENLA	Q52kk7 xenopus lae	973	161	8.9	1357	2	Q5MD89_BRARE	Q5md89 brachydanio
901	165	9.1	584	2	Q9Y3Y8_HUMAN	Q9y3y8 homo sapien	974	161	8.9	2541	2	Q19663_CAEBL	Q19663 caenorhabdi
902	165	9.1	822	1	FGFR1_MOUSE	P16092 mus musculu	975	160.5	8.9	422	2	Q86CY9_HELAN	Q86cy9 helicoverpa
903	165	9.1	822	1	FGFR1_RAT	Q04589 rattus norv	976	160.5	8.9	646	2	Q8NHN8_HUMAN	Q8nhn8 homo sapien
904	165	9.1	822	2	Q60818_MOUSE	Q60818 mus musculu	977	160.5	8.9	646	2	Q9N812_HUMAN	Q9n812 homo sapien
905	165	9.1	998	2	Q9W4Y6_DROME	Q9w4y6 drosophila	978	160.5	8.9	980	1	CSFIR1_FELCA	P13369 felle silve
906	165	9.1	1014	2	Q8NFA6_HUMAN	Q8nfa6 homo sapien	979	160.5	8.9	1237	2	Q610C8_CAEBR	Q610c8 caenorhabdi
907	165	9.1	2222	2	Q97394_DROME	Q97394 drosophila	980	160	8.9	319	1	GPA33_HUMAN	Q99795 homo sapien

981	160	8.9	319	2	Q5VZP6_HUMAN	Q5VZP6 homo sapien	1054	156.5	8.7	799	2	Q8CIB8_MOUSE	Q8CIB8 mus musculus
982	160	8.9	491	2	Q5ONS6_BRARE	Q5ONS6 brachydanio	1055	156.5	8.7	811	2	Q9YH43_XENLA	Q9YH43 xenopus lae
983	160	8.9	544	2	Q7Z285_BRARE	Q7Z285 brachydanio	1056	156.5	8.7	1292	2	Q4RHM3_TETNG	Q4RHM3 tetraodon n
984	160	8.5	564	1	CD166_BRARE	Q90460 brachydanio	1057	156	8.6	692	2	Q800Y3_BRARE	Q800Y3 brachydanio
985	160	8.9	564	2	Q6IQX4_BRARE	Q6IQX4 brachydanio	1058	156	8.6	740	2	Q96P29_HUMAN	Q96P29 homo sapien
986	160	8.9	640	2	Q8BSM2_MOUSE	Q8BSM2 mus musculus	1059	156	8.6	756	2	Q800Z0_BRARE	Q800Z0 brachydanio
987	160	8.9	822	1	FGFR1_HUMAN	P11362 homo sapien	1060	156	8.6	977	1	CSF1R_MOUSE	P09581 mus musculus
988	160	8.9	1144	2	Q18100_CABEL	Q18100 caenorhabdi	1061	156	8.6	978	1	CSF1R_RAT	Q00495 rattus norv
989	160	8.9	1147	2	Q53U86_CABEL	Q53U86 caenorhabdi	1062	156	8.6	1238	2	Q4S5S6_TETNG	Q4S5S6 tetraodon n
990	160	8.9	1437	2	Q44329_HIRME	Q44329 hirudo medi	1063	156	8.6	1501	2	Q7KUK9_DROME	Q7KUK9 drosophila
991	160	8.9	6839	2	Q23550_CABEL	Q23550 caenorhabdi	1064	156	8.6	7158	2	Q23551_CABEL	Q23551 caenorhabdi
992	159.5	8.8	570	2	Q8NCE6_HUMAN	Q8NCE6 homo sapien	1065	155.5	8.6	761	2	Q95LQ2_MACFA	Q95LQ2 macaca fasc
993	159.5	8.8	585	1	CEA20_HUMAN	Q6UY09 homo sapien	1066	155.5	8.6	797	2	Q52V40_BRAFL	Q52V40 branchiosto
994	159.5	8.8	975	2	Q97174_DROME	Q97174 drosophila	1067	155.5	8.6	880	1	TVRO3_MOUSE	P55144 mus musculus
995	159	8.8	226	2	Q7PUJ2_ANOGA	Q7PUJ2 anopheles g	1068	155.5	8.6	880	2	Q6NZM6_MOUSE	Q6NZM6 mus musculus
996	159	8.8	346	2	Q4PKP5_BRARE	Q4PKP5 brachydanio	1069	155	8.6	226	2	Q4RDM1_TETNG	Q4RDM1 tetraodon n
997	159	8.8	816	2	Q91285_PLEWA	Q91285 pleurodeles	1070	155	8.6	373	2	Q9H6B4_HUMAN	Q9H6B4 homo sapien
998	159	8.8	973	2	Q7QJK6_ANOGA	Q7QJK6 anopheles g	1071	155	8.6	454	2	Q91W54_MOUSE	Q91W54 mus musculus
999	159	8.8	1209	2	Q4SFS8_TETNG	Q4SFS8 tetraodon n	1072	155	8.6	458	2	Q61351_MOUSE	Q61351 mus musculus
1000	159	8.8	1272	2	Q5GIT3_BRARE	Q5GIT3 brachydanio	1073	155	8.6	521	1	CEAM1_MOUSE	P31809 mus musculus
1001	159	8.8	1948	1	PTPR3_HUMAN	Q13332 homo sapien	1074	155	8.6	521	2	Q61352_MOUSE	Q61352 mus musculus
1002	159	8.8	2696	2	Q60WB1_CABER	Q60WB1 caenorhabdi	1075	155	8.6	540	2	Q925P3_MOUSE	Q925P3 mus musculus
1003	158.5	8.8	211	2	Q7QBC5_ANOGA	Q7QBC5 anopheles g	1076	155	8.6	540	2	Q4RRTP9_TETNG	Q4RRTP9 tetraodon n
1004	158.5	8.8	388	1	BASI_CHICK	P17790 gallus gall	1077	155	8.6	677	2	Q7PMJ1_ANOGA	Q7PMJ1 anopheles g
1005	158.5	8.8	683	2	Q5TTJ6_ANOGA	Q5TTJ6 anopheles g	1078	155	8.6	699	2	Q4RT82_TETNG	Q4RT82 tetraodon n
1006	158.5	8.8	862	2	Q4SNP3_TETNG	Q4SNP3 tetraodon n	1079	155	8.6	819	1	FGFR1_CHICK	P21804 gallus gall
1007	158.5	8.8	912	1	ICAM5_RABIT	Q28730 oryctolagus	1080	155	8.6	977	2	Q96RD3_HUMAN	Q96RD3 homo sapien
1008	158.5	8.8	1199	2	Q21041_CABEL	Q21041 caenorhabdi	1081	155	8.6	1343	2	Q5PQU0_RAT	Q5PQU0 rattus norv
1009	158.5	8.8	1215	2	Q7KTI7_DROME	Q7KTI7 drosophila	1082	155	8.6	1363	1	VGPR3_MOUSE	P35917 mus musculus
1010	158.5	8.8	1278	2	Q4SW90_TETNG	Q4SW90 tetraodon n	1083	155	8.6	1363	1	Q5SU94_MOUSE	Q5SU94 mus musculus
1011	158.5	8.8	1461	2	Q8T9F6_DROME	Q8T9F6 drosophila	1084	155	8.6	1367	1	VGPR2_MOUSE	P35918 mus musculus
1012	158.5	8.8	1474	2	Q8T4M0_DROME	Q8T4M0 drosophila	1085	154.5	8.6	257	2	Q4S0M3_TETNG	Q4S0M3 tetraodon n
1013	158.5	8.8	1503	2	Q7KTI8_DROME	Q7KTI8 drosophila	1086	154.5	8.6	602	1	NRG1_CHICK	Q05199 gallus gall
1014	158.5	8.8	1509	2	Q9VLQ8_DROME	Q9VLQ8 drosophila	1087	154.5	8.6	1387	2	Q4SQU3_TETNG	Q4SQU3 tetraodon n
1015	158.5	8.8	1509	2	Q8IPG1_DROME	Q8IPG1 drosophila	1088	154.5	8.6	1897	1	PTPRF_HUMAN	P10586 homo sapien
1016	158	8.7	286	2	Q7QC80_ANOGA	Q7QC80 anopheles g	1089	154.5	8.6	1898	2	Q8GWS0_HUMAN	Q8GWS0 homo sapien
1017	158	8.7	302	2	Q5TPA7_ANOGA	Q5TPA7 anopheles g	1090	154.5	8.6	1898	2	Q5T021_HUMAN	Q5T021 homo sapien
1018	158	8.7	360	2	Q61565_MOUSE	Q61565 mus musculus	1091	154.5	8.6	1907	2	Q5T022_HUMAN	Q5T022 homo sapien
1019	158	8.7	361	2	Q9QW79_MUR1	Q9QW79 mus sp. fib	1092	154.5	8.6	1918	2	Q5W9G2_HUMAN	Q5W9G2 tetraodon n
1020	158	8.7	820	2	Q53H63_HUMAN	Q53H63 mus sapien	1093	154.5	8.6	2095	2	Q4RYE5_TETNG	Q4RYE5 tetraodon n
1021	158	8.7	822	2	Q9QV77_MUR1	Q9QV77 rattus sp.	1094	154	8.5	549	2	Q9D006_MOUSE	Q9D006 mus musculus
1022	157.5	8.7	346	2	Q9CTL3_MOUSE	Q9CTL3 mus musculus	1095	154	8.5	606	2	Q9ESS7_MOUSE	Q9ESS7 mus musculus
1023	157.5	8.7	441	2	Q8C139_MOUSE	Q8C139 mus musculus	1096	154	8.5	624	2	Q9ESS6_RAT	Q9ESS6 rattus norv
1024	157.5	8.7	496	1	MYOT1_MOUSE	Q9JF19 mus musculus	1097	154	8.5	648	2	Q9EPF1_MOUSE	Q9EPF1 mus musculus
1025	157.5	8.7	531	2	Q7QBY7_ANOGA	Q7QBY7 anopheles g	1098	154	8.5	648	2	Q8R2Y2_MOUSE	Q8R2Y2 mus musculus
1026	157.5	8.7	583	1	CD166_MOUSE	Q61490 mus musculus	1099	154	8.5	686	1	IRPL2_HUMAN	Q8R2Y2 h x-linked
1027	157.5	8.7	583	2	Q54AJ5_MOUSE	Q54AJ5 mus musculus	1100	154	8.5	686	2	Q5H9L9_HUMAN	Q5H9L9 homo sapien
1028	157.5	8.7	697	1	SIG10_HUMAN	Q961C7 homo sapien	1101	154	8.5	816	2	Q8GPM4_HYDAT	Q8GPM4 hydrattis co
1029	157.5	8.7	939	2	Q967X6_DROME	Q967X6 drosophila	1102	154	8.5	1348	1	VGPR2_COTJA	P52583 coturnix co
1030	157.5	8.7	939	2	Q9VB35_DROME	Q9VB35 drosophila	1103	154	8.5	1919	2	Q7QCP0_ANOGA	Q7QCP0 anopheles g
1031	157.5	8.7	978	1	KFMS_FSVMD	F00345 feline sarc	1104	153.5	8.5	1233	2	Q7QBV1_ANOGA	Q7QBV1 tetraodon n
1032	157.5	8.7	1376	2	Q5DTJ9_MOUSE	Q5DTJ9 mus musculus	1105	153.5	8.5	226	2	Q4T419_TETNG	Q4T419 tetraodon n
1033	157.5	8.7	1503	2	Q8T4L8_DROME	Q8T4L8 drosophila	1106	153.5	8.5	280	2	Q93350_CABEL	Q93350 caenorhabdi
1034	157	8.7	298	1	JAM1_BOVIN	Q9XT56 bos taurus	1107	153.5	8.5	510	2	Q5E929_BOVIN	Q5E929 bos taurus
1035	157	8.7	298	2	Q5E9V8_BOVIN	Q5E9V8 bos taurus	1108	153.5	8.5	1173	2	Q6NR54_DROME	Q6NR54 drosophila
1036	157	8.7	299	1	JAM1_HUMAN	Q9Y624 homo sapien	1109	153.5	8.5	1905	2	Q5VVL9_HUMAN	Q5VVL9 homo sapien
1037	157	8.7	299	2	Q6F1B4_HUMAN	Q6F1B4 homo sapien	1110	153.5	8.5	2217	2	Q8AV57_CHICK	Q8AV57 gallus gall
1038	157	8.7	383	2	Q75ML9_HUMAN	Q75ML9 homo sapien	1111	153.5	8.5	6048	2	Q7QPM9_ANOGA	Q7QPM9 anopheles g
1039	157	8.7	446	2	Q63236_RAT	Q63236 rattus norv	1112	153	8.5	686	2	Q7QPM9_ANOGA	Q7QPM9 anopheles g
1040	157	8.7	527	2	Q4SZU1_TETNG	Q4SZU1 tetraodon n	1113	153	8.5	977	2	Q5VYK9_HUMAN	Q5VYK9 homo sapien
1041	157	8.7	641	2	Q86SD2_CIOIN	Q86SD2 ciona intes	1114	153	8.5	1108	2	Q5RJH4_MOUSE	Q5RJH4 mus musculus
1042	157	8.7	707	2	Q5VXZ8_HUMAN	Q5VXZ8 homo sapien	1115	153	8.5	1348	2	Q677M1_CHICK	Q677M1 gallus gall
1043	157	8.7	734	2	Q96LA4_HUMAN	Q96LA4 homo sapien	1116	153	8.5	1788	2	Q91AJ0_XENLA	Q91AJ0 xenopus lae
1044	157	8.7	734	2	Q96P31_HUMAN	Q96P31 homo sapien	1117	153	8.5	1912	1	PTPRD_HUMAN	P23468 homo sapien
1045	157	8.7	742	2	Q8N6S2_HUMAN	Q8N6S2 homo sapien	1118	152.5	8.4	347	2	Q6PJ52_HUMAN	Q6PJ52 homo sapien
1046	157	8.7	1272	2	Q4JDD5_BRARE	Q4JDD5 brachydanio	1119	152.5	8.4	509	2	Q9EQY5_MOUSE	Q9EQY5 mman-g pr
1047	157	8.7	6710	2	Q61SF4_CABER	Q61SF4 caenorhabdi	1120	152.5	8.4	519	1	CEAM1_RAT	P16573 rattus norv
1048	156.5	8.7	400	2	Q4T054_TETNG	Q4T054 tetraodon n	1121	152.5	8.4	1484	2	Q5W9G3_HUMAN	Q5W9G3 homo sapien
1049	156.5	8.7	416	1	RAGE_BOVIN	Q28173 bos taurus	1122	152.5	8.4	1802	2	Q28633_RABIT	Q28633 oryctolagus
1050	156.5	8.7	473	2	Q5PEW7_XENLA	Q5PEW7 xenopus lae	1123	152.5	8.4	2290	2	Q4S6A6_TETNG	Q4S6A6 tetraodon n
1051	156.5	8.7	753	2	Q5J7D9_MOUSE	Q5J7D9 mus musculus	1124	152.5	8.4	7105	2	Q7FXW9_ANOGA	Q7FXW9 anopheles g
1052	156.5	8.7	797	2	Q52V39_BRAFL	Q52V39 branchiosto	1125	152	8.4	369	2	Q5VJ70_RAT	Q5VJ70 rattus norv
1053	156.5	8.7	799	2	Q8C3V5_MOUSE	Q8C3V5 mus musculus	1126	152	8.4	476	2	Q4R4S1_MACFA	Q4R4S1 macaca fasc

1127	152	8.4	617	2	Q51F12_BRARE	Q51f12 brachydanio	1200	149	8.3	372	2	Q8K1G0_RAT	Q8k1g0 rattus norv
1128	152	8.4	617	2	Q5M544_BRARE	Q5m544 brachydanio	1201	149	8.3	373	2	Q8R373_MOUSE	Q8r373 mus musculus
1129	152	8.4	620	2	Q4S1C0_TETNG	Q4s1c0 tetraodon n	1202	149	8.3	388	2	Q9Z151_MOUSE	Q9z151 mus musculus
1130	152	8.4	636	2	Q22040_CAEBL	Q22040 caenorhabdi	1203	149	8.3	483	2	Q4RRK0_TETNG	Q4rrk0 tetraodon n
1131	152	8.4	687	2	Q9S008_RAT	Q9s008 rattus norv	1204	149	8.3	570	2	Q6GLY1_XENLA	Q6gl11 xenopus lae
1132	152	8.4	772	2	Q5NKT7_PANTR	Q5nkt7 pan troglod	1205	149	8.3	1843	2	Q4Sff7_TETNG	Q4sff7 tetraodon n
1133	152	8.4	783	2	Q86T42_HUMAN	Q86t42 homo sapien	1206	149	8.3	1894	1	PTPRD_MOUSE	Q64487 mus musculus
1134	152	8.4	810	2	Q7PUH1_ANOGA	Q7puh1 anopheles g	1207	148.5	8.2	220	2	Q7PX67_ANOGA	Q7px67 anopheles g
1135	152	8.4	880	1	TYRO3_RAT	P55146 rattus norv	1208	148.5	8.2	260	2	Q4S8Z8_TETNG	Q4s8z8 tetraodon n
1136	152	8.4	1024	2	Q63HJ3_HUMAN	Q63hj3 homo sapien	1209	148.5	8.2	289	2	Q7ZWT0_XENLA	Q7zwt0 xenopus lae
1137	152	8.4	1092	2	Q91ZT0_RAT	Q91zt0 rattus norv	1210	148.5	8.2	476	2	Q7ZAJ8_XENLA	Q7zaj8 xenopus lae
1138	152	8.4	1123	2	Q659K7_HUMAN	Q659k7 homo sapien	1211	148.5	8.2	521	1	CD166_CANFA	Q46634 canle famli
1139	152	8.4	1141	1	MYPC1_HUMAN	Q00872 homo sapien	1212	148.5	8.2	536	2	Q9GV82_DROME	Q9gv82 drosophila
1140	152	8.4	1141	2	Q8N3L2_HUMAN	Q8n3l2 homo sapien	1213	148.5	8.2	574	2	Q58EG3_BRARE	Q58eg3 brachydanio
1141	152	8.4	1148	2	Q8N3R4_HUMAN	Q8n3r4 homo sapien	1214	148.5	8.2	588	1	CD166_CHICK	P42292 gallus gall
1142	152	8.4	1148	2	Q86T39_HUMAN	Q86t39 homo sapien	1215	148.5	8.2	673	2	Q6MZW2_HUMAN	Q6mzw2 homo sapien
1143	152	8.4	1171	2	Q86TC8_HUMAN	Q86tc8 homo sapien	1216	148.5	8.2	821	2	Q9YH44_XENLA	Q9yh44 xenopus lae
1144	152	8.4	1171	2	Q86TAB_HUMAN	Q86tab homo sapien	1217	148.5	8.2	1173	2	Q9V7J8_DROME	Q9v7j8 drosophila
1145	152	8.4	1343	1	VGFR2_RAT	Q08775 rattus norv	1218	148.5	8.2	1192	2	Q610E4_CAEBR	Q610e4 caenorhabdi
1146	152	8.4	1363	2	Q91ZT1_RAT	Q91zt1 rattus norv	1219	148.5	8.2	1497	2	Q5XJY4_MOUSE	Q5xjy4 mus musculus
1147	151.5	8.4	229	2	Q7PUC4_ANOGA	Q7puc4 anopheles g	1220	148.5	8.2	1501	2	Q7TT17_MOUSE	Q7tt17 mus musculus
1148	151.5	8.4	344	1	CEAM6_HUMAN	P40199 homo sapien	1221	148.5	8.2	1502	2	Q9UM81_HUMAN	Q9um81 homo sapien
1149	151.5	8.4	344	2	Q53XP7_HUMAN	Q53xp7 homo sapien	1222	148.5	8.2	1560	2	Q59FX6_HUMAN	Q59fx6 homo sapien
1150	151.5	8.4	344	2	Q13774_HUMAN	Q13774 homo sapien	1223	148.5	8.2	1887	2	Q9QW67_9MURI	Q9qw67 rattus norv
1151	151.5	8.4	459	2	Q4RS41_TETNG	Q4rs41 tetraodon n	1224	148.5	8.2	1904	2	Q64699_MOUSE	Q64699 mus musculus
1152	151.5	8.4	564	2	Q7ZU00_BRARE	Q7zu00 brachydanio	1225	148.5	8.2	1907	2	Q4JFC7_MOUSE	Q4jfc7 mus musculus
1153	151.5	8.4	847	1	FSTL5_MOUSE	Q8bfz2 mus musculus	1226	148	8.2	622	2	Q9JKB2_MOUSE	Q9jkb2 mus musculus
1154	151.5	8.4	948	2	Q9Ttd7_TRIVU	Q9ttc7 trichosurus	1227	148	8.2	694	2	Q8SWT7_DROME	Q8swt7 drosophila
1155	151.5	8.4	1898	2	Q9EQ17_MOUSE	Q9eq17 mus musculus	1228	148	8.2	709	2	Q8IXC7_HUMAN	Q8ixc7 homo sapien
1156	151	8.4	402	2	Q5UE88_CAEBL	Q5ue88 caenorhabdi	1229	148	8.2	821	2	Q4S2G2_TETNG	Q4s2g2 tetraodon n
1157	151	8.4	413	2	Q699P0_ANTPE	Q699p0 antherea p	1230	148	8.2	901	2	Q4SBD4_TETNG	Q4sbd4 tetraodon n
1158	151	8.4	497	2	Q4RFF7_TETNG	Q4rf7 tetraodon n	1231	147.5	8.2	318	2	Q91664_XENLA	Q91664 xenopus lae
1159	151	8.4	814	2	Q59H40_HUMAN	Q59h40 homo sapien	1232	147.5	8.2	331	2	Q63239_RAT	Q63239 rattus norv
1160	151	8.4	1156	2	Q676C3_9UROC	Q676c3 oikopleura	1233	147.5	8.2	403	1	RAGE_MOUSE	Q62151 mus musculus
1161	151	8.4	1367	2	Q7PQF4_ANOGA	Q7pqf4 anopheles g	1234	147.5	8.2	446	2	Q63237_RAT	Q63237 rattus norv
1162	150.5	8.3	208	2	Q4RK89_TETNG	Q4rk89 tetraodon n	1235	147.5	8.2	573	2	Q6GN50_XENLA	Q6gn50 xenopus lae
1163	150.5	8.3	417	2	Q4S916_TETNG	Q4s916 tetraodon n	1236	147.5	8.2	817	2	Q4H2M8_CIOIN	Q4h2m8 ciona intes
1164	150.5	8.3	437	2	Q8NF56_HUMAN	Q8nf56 homo sapien	1237	147.5	8.2	1499	2	Q90815_CHICK	Q90815 gallus gall
1165	150.5	8.3	509	2	Q91YK7_MOUSE	Q91yk7 mus musculus	1238	147.5	8.2	4194	2	Q61S53_CAEBR	Q61s53 caenorhabdi
1166	150.5	8.3	510	2	Q96KL5_HUMAN	Q96kl5 homo sapien	1239	147	8.1	262	2	Q5U9P8_PLOIN	Q5u9p8 plodia inte
1167	150.5	8.3	510	2	Q66NY8_HUMAN	Q66ny8 homo sapien	1240	147	8.1	402	2	Q3S444_MOUSE	Q3s444 mus musculus
1168	150.5	8.3	649	2	Q59F24_HUMAN	Q59f24 homo sapien	1241	147	8.1	549	2	Q9NQS3_HUMAN	Q9ngq3 homo sapien
1169	150.5	8.3	739	2	Q60NV9_CAEBR	Q60nv9 caenorhabdi	1242	147	8.1	739	1	PECA1_BOVIN	P51866 bos taurus
1170	150.5	8.3	747	2	Q5D7Z4_MOUSE	Q5dtz4 mus musculus	1243	147	8.1	1044	2	Q961W3_HUMAN	Q961w3 homo sapien
1171	150.5	8.3	824	2	Q90749_CHICK	Q90749 gallus gall	1244	147	8.1	1237	2	Q75147_HUMAN	Q75147 homo sapien
1172	150.5	8.3	875	2	Q4RKK6_TETNG	Q4rk6 tetraodon n	1245	147	8.1	1252	2	Q9JL11_MOUSE	Q9jll1 mus musculus
1173	150.5	8.3	888	2	Q7ZWM9_XENLA	Q7zwm9 xenopus lae	1246	146.5	8.1	291	2	Q6S8Q7_HUMAN	Q6s8q7 homo sapien
1174	150.5	8.3	961	1	ROB04_RAT	Q80w87 rattus norv	1247	146.5	8.1	326	2	Q8NC17_BOMMO	Q8nc17 bombyx mori
1175	150.5	8.3	1047	2	Q4RG7_TETNG	Q4rg7 tetraodon n	1248	146.5	8.1	468	2	Q9XY08_BOMMO	Q9xy08 bombyx mori
1176	150.5	8.3	1065	1	Q4RH24_TETNG	Q4rh24 tetraodon n	1249	146.5	8.1	484	2	Q99J08_MOUSE	Q99j08 mus musculus
1177	150.5	8.3	1298	1	VGFR3_HUMAN	P35916 homo sapien	1250	146.5	8.1	606	2	Q9ESS8_RAT	Q9es8 rattus norv
1178	150.5	8.3	1298	2	Q86W08_HUMAN	Q86w08 homo sapien	1251	146.5	8.1	648	2	Q9EPF2_RAT	Q9epf2 rattus norv
1179	150.5	8.3	1363	2	Q86W07_HUMAN	Q86w07 homo sapien	1252	146.5	8.1	847	1	FSTL5_HUMAN	Q8n475 homo sapien
1180	150.5	8.3	1478	2	Q59H90_HUMAN	Q59h90 homo sapien	1253	146.5	8.1	1111	2	Q5BJ14_BRARE	Q5bj14 brachydanio
1181	150	8.3	296	2	Q59DX6_DROME	Q59dx6 drosophila	1254	146.5	8.1	1280	2	Q9EPX2_MOUSE	Q9epx2 mus musculus
1182	150	8.3	323	2	Q5U198_DROME	Q5u198 drosophila	1255	146.5	8.1	1903	2	Q5SPJ6_MOUSE	Q5spj6 mus musculus
1183	150	8.3	343	2	Q7TP22_RAT	Q7tp22 rattus norv	1256	146	8.1	486	2	Q8CCH8_MOUSE	Q8cch8 mus musculus
1184	150	8.3	686	1	IRPL2_MOUSE	Q9er86 mus musculus	1257	146	8.1	549	2	Q9JLB9_MOUSE	Q9jlb9 mus musculus
1185	150	8.3	711	2	Q24205_DROME	Q24205 drosophila	1258	146	8.1	738	2	P79390_BOEPR	P79390 bos primige
1186	150	8.3	977	2	Q6NXV8_MOUSE	Q6nxv8 mus musculus	1259	146	8.1	782	2	Q61563_MOUSE	Q61563 mus musculus
1187	150	8.3	1171	2	Q86T48_HUMAN	Q86t48 homo sapien	1260	146	8.1	790	2	Q8C4N3_MOUSE	Q8c4n3 mus musculus
1188	149.5	8.3	173	2	Q7PSS8_ANOGA	Q7pss8 anopheles g	1261	146	8.1	827	1	NTRK3_CHICK	Q91044 gallus gall
1189	149.5	8.3	349	1	CEAM8_HUMAN	P31997 homo sapien	1262	146	8.1	867	2	Q59DZ1_DROME	Q59dz1 drosophila
1190	149.5	8.3	360	2	Q8BJ10_MOUSE	Q8bj10 mus musculus	1263	146	8.1	1087	2	Q7ZY71_XENLA	Q7zy71 xenopus lae
1191	149.5	8.3	739	1	VCAM1_RAT	P29534 rattus norv	1264	146	8.1	1088	1	PGFRA_MOUSE	P20786 rattus norv
1192	149.5	8.3	739	2	Q5FV53_RAT	Q5fv53 rattus norv	1265	146	8.1	1089	1	PGFRA_MOUSE	P26618 mus musculus
1193	149.5	8.3	815	2	Q805B9_BRARE	Q805b9 brachydanio	1266	146	8.1	1889	2	Q5TSJ3_MOUSE	Q5tsj3 mus musculus
1194	149.5	8.3	1073	2	Q9W1T8_DROME	Q9w1t8 drosophila	1267	145.5	8.1	188	2	Q5SZ11_HUMAN	Q5sz11 homo sapien
1195	149.5	8.3	1250	2	Q8TD18_HUMAN	Q8tdy8 homo sapien	1268	145.5	8.1	232	2	Q66172_BRARE	Q66172 brachydanio
1196	149.5	8.3	1501	2	Q9QW00_9MURI	Q9qw00 rattus sp.	1269	145.5	8.1	391	2	Q4S871_TETNG	Q4s871 tetraodon n
1197	149.5	8.3	1501	2	Q4JF18_RAT	Q4jfl8 rattus norv	1270	145.5	8.1	504	2	Q6NNA1_DROME	Q6nnal drosophila
1198	149.5	8.3	1863	2	Q64605_RAT	Q64605 rattus norv	1271	145.5	8.1	508	2	Q9VGD2_DROME	Q9vgd2 drosophila
1199	149	8.3	335	2	Q75237_HUMAN	Q75237 homo sapien	1272	145.5	8.1	520	2	Q925P2_MOUSE	Q925p2 mus musculus

1273	145.5	8.1	664	2	Q9VGD3_DROME	O9vdg3 drosophila	1346	142	7.9	1252	2	Q9EQS9_MOUSE	Q9eqs9 mus musculus
1274	145.5	8.1	713	2	Q4SSE0_TETNG	O4s8e0 tetraodon n	1347	142	7.9	1253	2	Q9EQS8_MOUSE	Q9eqs8 mus musculus
1275	145.5	8.1	739	1	VCAM1_MOUSE	F29533 mus musculus	1348	142	7.9	1254	2	Q60ZNS_CAEER	Q60zn5 caenorhabdi
1276	145.5	8.1	739	1	VCAM1_MOUSE	O91X98 mus musculus	1349	141.5	7.8	324	2	Q6UPK9_HUMAN	Q6upk9 homo sapien
1277	145.5	8.1	808	1	FGFR4_MOUSE	O03142 mus musculus	1350	141.5	7.8	333	2	Q75238_HUMAN	O75238 homo sapien
1278	145.5	8.1	831	2	Q71SV9_CHICK	O71sv9 gallus gall	1351	141.5	7.8	881	2	Q965M2_CAEEL	Q965m2 caenorhabdi
1279	145.5	8.1	1012	1	ROBO4_MOUSE	O8c310 mus musculus	1352	141.5	7.8	953	1	UNC5D_HUMAN	Q6uxz4 homo sapien
1280	145.5	8.1	1898	2	Q64604_RAT	O64604 rattus norv	1353	141.5	7.8	1007	1	ROBO4_HUMAN	Q8wz75 homo sapien
1281	145	8.0	241	2	Q4T426_TETNG	O4t426 tetraodon n	1354	141.5	7.8	1227	2	Q21038_CAEEL	Q21038 caenorhabdi
1282	145	8.0	259	2	Q9Y5B2_HUMAN	O9y5b2 homo sapien	1355	141.5	7.8	2000	2	Q97791_RABIT	O97791 oryctolagus
1283	145	8.0	362	2	Q4T2X1_TETNG	O4t2x1 tetraodon n	1356	141	7.8	276	2	Q6P0R7_BRARE	Q6p0r7 brachydanio
1284	145	8.0	373	2	Q920S5_MOUSE	O920s5 mus musculus	1357	141	7.8	303	2	Q4SF99_TETNG	Q4sf99 tetraodon n
1285	145	8.0	622	2	Q9ESS5_MOUSE	O9ess5 mus musculus	1358	141	7.8	308	2	Q503N7_BRARE	Q503n7 brachydanio
1286	145	8.0	725	2	Q59HE0_HUMAN	O59he0 homo sapien	1359	141	7.8	338	2	Q6DHD4_BRARE	Q6dhd4 brachydanio
1287	145	8.0	782	2	Q8MTZ3_RABIT	O8mtz3 oryctolagus	1360	141	7.8	356	2	Q5SDZ4_DROME	Q5sdz4 drosophila
1288	145	8.0	812	2	Q8M257_DROME	O8m257 drosophila	1361	141	7.8	432	2	Q6DDE7_XENLA	Q6dde7 xenopus lae
1289	145	8.0	878	2	Q9GV22_MYTGA	O9gv22 mytilus gal	1362	141	7.8	456	2	Q7FUM9_ANOGA	Q7fum9 anopheles g
1290	145	8.0	949	2	Q4RHT4_TETNG	O4rht4 tetraodon n	1363	141	7.8	626	2	Q6DCH3_XENLA	Q6dch3 xenopus lae
1291	145	8.0	972	1	CSF1R_HUMAN	P07333 homo sapien	1364	141	7.8	815	2	O8AVP3_BRARE	Q8avp3 brachydanio
1292	145	8.0	972	2	Q86VW7_HUMAN	O86vw7 homo sapien	1365	141	7.8	819	2	Q4T5K0_TETNG	Q4t5k0 tetraodon n
1293	145	8.0	1389	2	Q4VA61_MOUSE	Q4va61 mus musculus	1366	141	7.8	821	1	FGFR2_HUMAN	F21802 homo sapien
1294	144.5	8.0	421	2	Q9NBB2_DROME	O9nbb2 drosophila	1367	141	7.8	879	2	Q8V199_RAT	Q8v199 rattus norv
1295	144.5	8.0	559	2	Q7PSH7_ANOGA	O7psh7 anopheles g	1368	141	7.8	888	2	Q8V1A0_RAT	Q8v1a0 rattus norv
1296	144.5	8.6	606	2	Q6IRH8_RAT	O6irh8 rattus norv	1369	141	7.8	977	2	Q98SUI_9TELE	Q98sui danio nigro
1297	144.5	8.0	739	2	Q8K0X1_MOUSE	O8k0x1 mus musculus	1370	140.5	7.8	390	2	Q4S8T4_TETNG	Q4s8t4 tetraodon n
1298	144.5	8.0	754	2	Q8BZ76_MOUSE	O8bz76 m mus muscu	1371	140.5	7.8	413	2	Q4H1G8_SAMCR	Q4h1g8 samia cynth
1299	144.5	8.0	880	2	Q8QFP9_XENLA	O8qfp9 xenopus lae	1372	140.5	7.8	705	2	Q63710_RATRT	Q63710 rattus ratt
1300	144.5	8.0	1261	2	Q4JFL6_RAT	O4jfl6 rattus norv	1373	140.5	7.8	737	2	Q965M3_CAEEL	Q965m3 caenorhabdi
1301	144.5	8.0	1495	2	Q4JFL7_RAT	O4jfl7 rattus norv	1374	140.5	7.8	743	2	Q6P4H5_HUMAN	Q6p4h5 homo sapien
1302	144.5	8.0	3094	2	Q4RE88_TETNG	O4re88 tetraodon n	1375	140.5	7.8	790	2	Q90699_CHICK	Q90699 gallus gall
1303	144	8.0	278	2	Q9QVL3_MOUSE	O9qvl3 mus musculus	1376	140.5	7.8	823	1	CEK3_CHICK	P18461 gallus gall
1304	144	8.0	413	2	Q6ZNI1_HUMAN	O6zni1 homo sapien	1377	140.5	7.8	1049	2	Q4S0F2_TETNG	Q4s0f2 tetraodon n
1305	144	8.0	422	2	Q8WR61_LYMDI	O8wr61 lymantria d	1378	140.5	7.8	1079	2	Q6E7G6_CANFA	Q6e7g6 canis famli
1306	144	8.0	434	2	Q6DN72_HUMAN	O6dn72 homo sapien	1379	140.5	7.8	1089	1	PGFRA_HUMAN	P16234 homo sapien
1307	144	8.0	438	2	Q9JLB7_MOUSE	O9jlb7 mus musculus	1380	140.5	7.8	2164	2	Q9IAR9_CHICK	Q9iar9 gallus gall
1308	144	8.0	444	2	Q5ZIA8_CHICK	O5zia8 gallus gall	1381	140	7.8	287	2	Q7Q894_ANOGA	Q7q894 anopheles g
1309	144	8.0	510	2	Q9JLB8_MOUSE	O9jlb8 mus musculus	1382	140	7.8	562	2	Q6VNR7_BRARE	Q6vnr7 brachydanio
1310	144	8.0	542	2	Q8NHN5_HUMAN	O8nhn5 homo sapien	1383	140	7.8	622	2	Q9R069_MOUSE	Q9r069 mus musculus
1311	144	8.0	891	2	Q25177_HYDAT	Q25177 hydra atten	1384	140	7.8	650	2	Q99K86_MOUSE	Q99k86 mus musculus
1312	143.5	7.9	296	2	Q64OC0_XENLA	Q64oc0 xenopus lae	1385	140	7.8	752	2	Q9XY84_HYDAT	Q9xy84 hydra atten
1313	143.5	7.9	300	2	Q7SYQ7_XENLA	O7syq7 xenopus lae	1386	140	7.8	800	2	Q99052_MOUSE	Q99052 mus musculus
1314	143.5	7.9	430	2	Q8NAF1_HUMAN	O8naf1 homo sapien	1387	140	7.8	800	2	Q7TSI8_MOUSE	Q7tsi8 mus musculus
1315	143.5	7.9	656	2	Q4SPF7_TETNG	O4spf7 tetraodon n	1388	140	7.8	800	2	Q9I8X3_BRARE	Q9i8x3 brachydanio
1316	143.5	7.9	1177	2	Q21391_CAEEL	O21391 caenorhabdi	1389	140	7.8	801	1	FGFR3_MOUSE	Q61851 mus musculus
1317	143.5	7.9	12268	2	Q8MQ08_CAEEL	Q8mq08 caenorhabdi	1390	140	7.8	879	1	FPRP_HUMAN	Q9p2b2 homo sapien
1318	143.5	7.9	13100	2	Q09165_CAEEL	O09165 caenorhabdi	1391	140	7.8	879	2	Q5VVU9_HUMAN	Q5vvu9 homo sapien
1319	143	7.9	310	2	Q4V8T3_BRARE	O4v8t3 brachydanio	1392	140	7.8	890	1	TYRO3_HUMAN	Q06418 homo sapien
1320	143	7.9	442	2	Q8C306_MOUSE	O8c306 mus musculus	1393	140	7.8	890	2	Q59VM9_HUMAN	Q59vm9 homo sapien
1321	143	7.9	620	1	SMP_COTJA	O92154 coturnix co	1394	140	7.8	951	2	Q59FM9_HUMAN	Q59fm9 homo sapien
1322	143	7.9	688	2	Q8KJH4_MOUSE	O8kjh4 mus musculus	1395	140	7.8	972	1	Q99662_HUMAN	Q99662 homo sapien
1323	143	7.9	688	2	Q55095_MOUSE	O55095 mus musculus	1396	140	7.8	976	2	Q99662_HUMAN	Q99662 homo sapien
1324	143	7.9	814	2	Q9VNP2_DROME	O9vnp2 drosophila	1397	140	7.8	976	2	Q61Q28_HUMAN	Q61q28 homo sapien
1325	143	7.9	972	2	Q761I0_CALJA	O761i0 callithrix	1398	140	7.8	2888	2	Q8MMK1_BOMMO	Q8mmk1 bombyx mori
1326	143	7.9	972	2	Q9I8N6_BRARE	O9i8n6 brachydanio	1399	140	7.8	3239	2	Q8T102_BOMMO	Q8t102 bombyx mori
1327	143	7.9	1011	2	Q24273_DROME	O24273 drosophila	1400	140	7.8	4203	2	Q965G2_CAEEL	Q965g2 caenorhabdi
1328	142.5	7.9	218	2	Q7Q385_ANOGA	Q7q385 anopheles g	1401	140	7.8	4219	2	Q9NL87_CAEEL	Q9nl87 caenorhabdi
1329	142.5	7.9	324	2	Q8NB18_HUMAN	O8nb18 homo sapien	1402	140	7.8	4250	2	Q5FY59_CAEEL	Q5fy59 caenorhabdi
1330	142.5	7.9	326	2	Q9UPK8_HUMAN	O9upk8 homo sapien	1403	140	7.8	4369	2	Q8MXD7_CAEEL	Q8mxd7 caenorhabdi
1331	142.5	7.9	435	1	PSG6_HUMAN	O00889 homo sapien	1404	140	7.8	4447	2	Q8MXD8_CAEEL	Q8mxd8 caenorhabdi
1332	142.5	7.9	461	2	Q5R1V2_BRARE	O5r1v2 brachydanio	1405	140	7.8	4889	1	Q9TXK2_CAEEL	Q9txk2 caenorhabdi
1333	142.5	7.9	515	2	Q96RE0_HUMAN	O96re0 homo sapien	1406	139.5	7.7	419	1	PSG1_HUMAN	P11464 homo sapien
1334	142.5	7.9	530	2	Q4RTW9_TETNG	O4rtw9 tetraodon n	1407	139.5	7.7	422	2	Q96PJ3_HUMAN	Q96pj3 homo sapien
1335	142.5	7.9	715	2	Q9NKA6_DROME	O9nka6 drosophila	1408	139.5	7.7	431	2	Q5DX21_HUMAN	Q5dx21 homo sapien
1336	142.5	7.9	739	1	VCAM1_HUMAN	P19320 homo sapien	1409	139.5	7.7	515	2	Q96PJ5_HUMAN	Q96pj5 homo sapien
1337	142.5	7.9	739	2	Q5R847_PONPY	O5r847 pongo pygma	1410	139.5	7.7	544	2	Q7Z197_XENLA	Q7z197 xenopus lae
1338	142.5	7.9	956	1	UNC5D_MOUSE	O8k1s2 mus musculus	1411	139.5	7.7	670	2	Q7ZZ47_BRARE	Q7zz47 brachydanio
1339	142.5	7.9	1019	2	Q8UVR8_FUGRU	O8uvr8 fugu rubrip	1412	139.5	7.7	696	2	Q5DU03_MOUSE	Q5du03 mus musculus
1340	142.5	7.9	1052	1	FGFR2_DROME	O09147 drosophila	1413	139.5	7.7	739	1	VCAM1_CANFA	Q28260 canis famli
1341	142	7.9	344	2	Q8WR42_CAEEL	O8wr42 caenorhabdi	1414	139.5	7.7	739	2	Q53FL7_HUMAN	Q53fl7 homo sapien
1342	142	7.9	345	2	Q8MPV0_CAEEL	O8mpv0 caenorhabdi	1415	139.5	7.7	743	2	Q6FIM7_HUMAN	Q6fim7 homo sapien
1343	142	7.9	494	2	Q9ESC6_MOUSE	O9esc6 mus musculus	1416	139.5	7.7	821	1	FGFR2_MOUSE	P21803 mus musculus
1344	142	7.9	505	2	Q9U965_GEOCY	O9u965 geodia cydo	1417	139.5	7.7	829	2	Q5TZ34_BRARE	Q5tz34 brachydanio
1345	142	7.9	806	1	CEK2_CHICK	P18460 gallus gall	1418	139.5	7.7	841	2	Q5STE3_MOUSE	Q5ste3 mus musculus

1419	139.5	7.7	850	2	Q4S3Y6_TETNG	Q4S3Y6 tetraodon n
1420	139.5	7.7	1200	2	Q676A1_9UROC	Q676a1 oikopleura
1421	139	7.7	250	2	Q611Y8_CABER	Q611y8 caenorhabdi
1422	139	7.7	343	2	Q5TRB7_ANOGA	Q5trb7 anopheles g
1423	139	7.7	403	2	Q6NZV3_BRARE	Q6nzv3 brachydanio
1424	139	7.7	416	2	Q96360_HYPCU	Q96360 hyphantria
1425	139	7.7	763	2	Q95YM9_HALRO	Q95ym9 halocynthia
1426	139	7.7	788	2	Q4QQP8_HUMAN	Q4qqp8 homo sapien
1427	139	7.7	824	2	Q91286_PLEWA	Q91286 pleurodeles
1428	139	7.7	976	2	Q5RID5_BRARE	Q5rid5 brachydanio
1429	139	7.7	976	2	Q9W755_BRARE	Q9w755 brachydanio
1430	138.5	7.7	151	2	Q4THV8_TETNG	Q4thv8 tetraodon n
1431	138.5	7.7	313	2	Q8UW13_LAPHA	Q8uw13 lapemis har
1432	138.5	7.7	336	2	Q4RU88_TETNG	Q4ru88 tetraodon n
1433	138.5	7.7	377	2	Q9VOY0_DROME	Q9vgy0 drosophila
1434	138.5	7.7	413	2	Q26438_HYACE	Q26438 hyalophora
1435	138.5	7.7	414	2	Q5VU13_HUMAN	Q5vul13 homo sapien
1436	138.5	7.7	419	2	Q96QL5_HUMAN	Q96ql5 homo sapien
1437	138.5	7.7	426	2	Q6ICR4_HUMAN	Q6icr4 homo sapien
1438	138.5	7.7	719	2	Q9U4G1_DROME	Q9u4g1 drosophila
1439	138.5	7.7	1896	2	Q9IAJ1_XENLA	Q9iaj1 xenopus lae
1440	138	7.6	135	2	Q7PLL7_DROME	Q7pll7 drosophila
1441	138	7.6	313	2	Q9U964_GEOCY	Q9u964 geodia cydo
1442	138	7.6	416	2	Q5T7G8_HUMAN	Q5t7g8 homo sapien
1443	138	7.6	515	1	PVR1_PIG	Q9g176 sus scrofa
1444	138	7.6	709	2	Q5T7G9_HUMAN	Q5t7g9 homo sapien
1445	138	7.6	767	2	Q86YC7_HUMAN	Q86yc7 homo sapien
1446	138	7.6	1087	1	PGFPA_XENLA	P26619 xenopus lae
1447	137.5	7.6	248	2	Q7PVM4_ANOGA	Q7pvm4 anopheles g
1448	137.5	7.6	353	2	Q4VMT0_XENLA	Q4vmt0 xenopus lae
1449	137.5	7.6	357	2	Q63238_RAT	Q63238 rattus norv
1450	137.5	7.6	385	2	Q9VKK8_DROME	Q9vkk8 drosophila
1451	137.5	7.6	413	1	HEMO_HYACE	P25033 hyalophora
1452	137.5	7.6	419	1	PSGA_HUMAN	Q00888 homo sapien
1453	137.5	7.6	428	2	Q9BRW2_HUMAN	Q9brw2 homo sapien
1454	137.5	7.6	432	2	Q52NV1_RAT	Q52nv1 rattus norv
1455	137.5	7.6	463	2	Q66J72_XENLA	Q66j72 xenopus lae
1456	137.5	7.6	501	2	Q4S2C5_TETNG	Q4s2c5 tetraodon n
1457	137.5	7.6	602	2	Q52NV2_RAT	Q52nv2 rattus norv
1458	137.5	7.6	740	1	PECA1_PIG	Q95242 sus scrofa
1459	137.5	7.6	977	2	Q98SU4_9TELE	Q98su4 danio albol
1460	137.5	7.6	1040	2	Q8NHN2_HUMAN	Q8nhn2 homo sapien
1461	137.5	7.6	1379	2	P79701_COTCO	Q179701 coturnix co
1462	137	7.6	283	2	Q7PCU3_ANOGA	Q7pcu3 anopheles g
1463	137	7.6	283	2	Q5TNQ2_ANOGA	Q5tnq2 anopheles g
1464	137	7.6	366	2	Q6NVZ3_HUMAN	Q6nvz3 homo sapien
1465	137	7.6	420	2	Q68DM9_HUMAN	Q68dm9 homo sapien
1466	137	7.6	424	1	PSG10_HUMAN	Q15235 homo sapien
1467	137	7.6	448	2	Q8IGA5_DROME	Q8iga5 drosophila
1468	137	7.6	448	2	Q9JHL7_RAT	Q9jhl7 rattus norv
1469	137	7.6	458	2	Q63093_RAT	Q63093 rattus norv
1470	137	7.6	459	2	Q9JHL6_RAT	Q9jhl6 rattus norv
1471	137	7.6	461	2	Q4RFF6_TETNG	Q4rfi6 tetraodon n
1472	137	7.6	517	1	PVRI_HUMAN	Q15223 homo sapien
1473	137	7.6	662	2	Q8MGZ9_DROME	Q8mgz9 drosophila
1474	137	7.6	662	2	Q9VGQ0_DROME	Q9vgq0 drosophila
1475	137	7.6	778	1	NTK1_CHICK	Q91009 gallus gall
1476	137	7.6	977	2	Q98SU2_DANKE	Q98su2 danio kerri
1477	136.5	7.6	459	2	Q86X91_HUMAN	Q86x91 homo sapien
1478	136.5	7.6	496	2	Q5EG09_ICTPU	Q5eg09 ictalurus p
1479	136.5	7.6	498	1	MYOTI_HUMAN	Q9ubf9 homo sapien
1480	136.5	7.6	677	2	Q8OHL2_CHICK	Q8ohl2 gallus gall
1481	136.5	7.6	738	1	PECA1_HUMAN	P16284 homo sapien
1482	136.5	7.6	838	2	Q4S4W8_TETNG	Q4s4w8 tetraodon n
1483	136.5	7.6	975	2	Q4LIN7_CARAU	Q4lin7 carassius a
1484	136.5	7.6	3100	2	Q7KYN5_HUMAN	Q7kyn5 homo sapien
1485	136	7.5	233	2	Q7Q9S4_ANOGA	Q7q9s4 anopheles g
1486	136	7.5	298	1	JAM2_MOUSE	Q9j159 mus musculus
1487	136	7.5	381	2	Q4SDA6_TETNG	Q4sda6 tetraodon n
1488	136	7.5	393	2	Q9S727_HUMAN	Q9s727 homo sapien
1489	136	7.5	903	2	Q8N9C0_HUMAN	Q8n9c0 homo sapien
1490	136	7.5	976	2	Q8JFR5_BRARE	Q8jfr5 brachydanio
1491	136	7.5	1122	2	Q4SAA1_TETNG	Q4saa1 tetraodon n

1492	135.5	7.5	218	2	Q7PJ18_ANOGA	Q7pj18 anopheles g
1493	135.5	7.5	326	2	Q9N166_PAPHA	Q9n166 papio hamad
1494	135.5	7.5	344	2	Q568F7_BRARE	Q568f7 brachydanio
1495	135.5	7.5	603	2	Q4SEN2_TETNG	Q4sen2 tetraodon n
1496	135.5	7.5	681	2	Q5DUF3_CHICK	Q5duf3 gallus gall
1497	135.5	7.5	762	2	Q71TW8_HUMAN	Q71tw8 homo sapien
1498	135.5	7.5	822	2	Q91288_PLEWA	Q91288 pleurodeles
1499	135.5	7.5	975	2	P79750_FUGRU	P79750 fugu rubrip
1500	135.5	7.5	13133	2	Q71A42_CAEBR	Q71a42 caenorhabdi

RESULT 1

Q5R554_PONPY PRELIMINARY; PRT; 344 AA.

AC Q5R554_PONPY

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DE Hypothetical protein DKFp459A2018.

GN Name=DKFp459A2018;

OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Pongo.

OX NCBI_TaxID=9600;

RP [1]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Cortex;

RG The German cDNA Consortium;

RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

RA Fobo G., Han M., Wiemann S.;

RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR861018; CAH93112.1; -; mRNA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 3.

DR SMART; SM00408; IGC2; 3.

DR PROSITE; PS00835; IG_LIKE; 3.

KW Hypothetical protein; Immunoglobulin domain.

SQ SEQUENCE 344 AA; 37998 MW; E766F477B31D288 CRC64;

Query Match 99.5%; Score 1797; DB 2; Length 344;

Best Local Similarity 99.4%; Pred. No. 1.4e-137;

Matches 342; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKTIQKWNHNSWAIETGLAALCLFGQVPRVSGDATFPKAMDNVTVRQESATLRCTID	60
Db	1	MKTIQKWNHNSWAIETGLAALCLFGQVPRVSGDATFPKAMDNVTVRQESATLRCTID	60
QY	61	NRVTRVLAWLNRSTLYAGNDKWLCDPRVLLSNTQTOYSIEIQNVDDVYDEGPYTCVSQTD	120
Db	61	NRVTRVLAWLNRSTLYAGNDKWLCDPRVLLSNTQTOYSIEIQNVDDVYDEGPYTCVSQTD	120
QY	121	NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHHSIPKAVGFV	180
Db	121	NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHHSIPKAVGFV	180
QY	181	SEDEYLEIQGITREOSGDYECASNVDVAAVPRVRKVTVNVPYIESEAKGTGVPVQOKGT	240
Db	181	SEDEYLEIQGITREOSGDYECASNVDVAAVPRVRKVTVNVPYIESEAKGTGVPVQOKGT	240
QY	241	LQCEASAVPSAEQWYKDDKRLIEGKKGVKVENRPFSLKLIFFNVSEHIDYGNITCVASNK	300
Db	241	LQCEASAVPSAEQWYKDDKRLIEGKKGVKVENRPFSLKLIFFNVSEHIDYGNITCVASNK	300
QY	301	LGHNTNASIMLFGPGAVSEVNGTSRRAGCVLLPLVLHLLLLKPF	344
Db	301	LGHNTNASIMLFGPGAVSEVNGTLRRAGCVLLPLVLHLLLLKPF	344

ALIGNMENTS

RESULT 1

Q5R554_PONPY	Q5R554_PONPY PRELIMINARY;	PRT;	344 AA.
ID	Q5R554;		
AC	Q5R554;		
DT	01-FEB-2005 (TrEMBLrel. 29, Created)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)		
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)		
DE	Hypothetical protein DKFZp459A2018.		
GN	Names=DKFZp459A2018;		
OS	Pongo pygmaeus (Orangutan).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Pongo.		
OX	NCBI_TaxID=9600;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Cortex;		
RG	The German cDNA Consortium;		
RA	Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,		
RA	Fobo G., Han M., Wiemann S.;		
RL	Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; CR861018; CAH93112.1; -; mRNA.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003598; IG_c2.		
DR	Pfam; PF00047; ig; 2.		
DR	SMART; SM00409; IG; 3.		
DR	SMART; SM00408; Igc2; 3.		
DR	PROSITE; PS50835; IG_LIKE; 3.		
KW	Hypothetical protein; Immunoglobulin domain.		
SQ	SEQUENCE 344 AA; 37998 MW; E766F477B31D288 CRC64;		
Query Match 99.5%; Score 1797; DB 2; Length 344;			
Best Local Similarity 99.4%; Pred. No. 1.4e-137;			
Matches 342; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MKTIOPKMNSISWALFTGLAALCLFGQVPVRSGDATFPKAMDNVTVROGESATLRCTID	60
Db	1	MKTIOPKMNSISWALFTGLAALCLFGQVPVRSGDATFPKAMDNVTVROGESATLRCTID	60
QY	61	NRVTRVAVLNRSTILYAGNDKWKCLDPVRVLLSNTQYISIEIQNVVDYDEGPTCSVQTD	120
Db	61	NRVTRVAVLNRSTILYAGNDKWKCLDPVRVLLSNTQYISIEIQNVVDYDEGPTCSVQTD	120
QY	121	NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVVRHISPKAVGFV	180
Db	121	NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVVRHISPKAVGFV	180
QY	181	SDEYLEIOGITREOSGDYECASNDVAAPVVRVKVTYVNPYPPISEAKGTGVPVQCKGT	240
Db	181	SDEYLEIOGITREOSGDYECASNDVAAPVVRVKVTYVNPYPPISEAKGTGVPVQCKGT	240
QY	241	LQCEASAVPSABFQWKDKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNK	300
Db	241	LQCEASAVPSABFQWKDKRLIEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNK	300
QY	301	LGHNTASIMLFGGAVSEVSGTSTRAGCWLLPLLVLLHLLKP	344
Db	301	LGHNTASIMLFGGAVSEVSGTSTRAGCWLLPLLVLLHLLKP	344

```

RESULT 2
QB8G333 MOUSE
ID QB8G333 MOUSE PRELIMINARY; PRT; 344 AA.
AC Q8BG337
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Mus musculus adult male corpora quadrigenima cDNA, RIKEN full-length
DE enriched library, clone:B230328N06 product:NEUROTRIMIN (GP65) homolog
DE (Mus musculus adult male corpora quadrigenima cDNA, RIKEN full-length
DE enriched library, clone:B23037K17 product:NEUROTRIMIN (GP65)
DE homolog).
GN Name=Hnt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenima;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai H., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenima;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaudo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuoka H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

```

```

RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenima;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenima;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigenima;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima J., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuoka T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; AK045973; BAC32555.1; -; mRNA.
DR EMBL; AK046377; BAC32695.1; -; mRNA.
DR HSSP; P13596; IQ21.
DR Ensembl; ENSMUSG00000059974; Mus musculus.
DR MGI; MGI:2446259; Hnt.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; Igc2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 344 AA; 37941 MW; CDA5299D4CD86065 CRC64;
Query Match 98.6%; Score 1780; DB 2; Length 344;
Best Local Similarity 98.0%; Pred. No. 3.5e-136;
Matches 337; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKTIQPKMNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVROGESATLRCTID 60
DB 1 MKTIQPKMNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVROGESATLRCTID 60
QY 61 NRVTAVLNRSTILYAGNDKCKLDPVVLLSNTQYSIEIQNVDDYDEGPTVCSVQTD 120

```

Db 61 NRVTNRVAVLNRSTLYAGNDKWCCLDPRVVLNNTQYQYIEIQNVVDVYDEGPTCSVQTD 120
QY 121 NHPKTSRVLHVQVSPKIVEISSDISINEGNISLTCIATGPEPTVWRHISPKVAGFV 180
DB 121 NHPKTSRVLHVQVSPKIVEISSDISINEGNISLTCIATGPEPTVWRHISPKVAGFV 180
QY 181 SEDEYLEIOGITREQSGDYECASNDVAAPVVRVVKVTYVNYPPYISEAKGTGVPVQKGT 240
DB 181 SEDEYLEIOGITREQSGDYECASNDVAAPVVRVVKVTYVNYPPYISEAKGTGVPVQKGT 240
QY 241 LOCEASAVPSAFQWKDKRLIEGKGVKVENRPFSLKILFPNVSEHDYGYNTCVASNK 300
DB 241 LOCEASAVPSAFQWKDKRLIEGKGVKVENRPFSLKILFPNVSEHDYGYNTCVASNK 300
QY 301 LGHTNASIMLFGGAVSEVSNGTSSRAGCVWLLPLVLHLLKLF 344
DB 301 LGHTNASIMLFGGAVSEVSNGTSSRAGCVWLLPLVLHLLKLF 344

RESULT 3
NTRI HUMAN STANDARD; PRT; 344 AA.
AC Q9P121; Q86VJ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Neurotrophin precursor (hNT)
GN Name=NT; ORFNames=UNQ297/PRO337;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandil R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROTEIN SEQUENCE OF 34-48.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoID=Q9P121-1; Sequence=Displayed;
CC Name=2;
CC IsoID=Q9P121-2; Sequence=VSP 010939;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoID=Q9P121-3; Sequence=VSP 010940, VSP 010941;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF126426; AAF37591.1; -; mRNA.
CC EMBL; AY358331; AAQ88697.1; -; mRNA.
CC EMBL; BC050716; AAH50716.1; -; mRNA.
CC HSSP; P13590; IIE5.
CC Ensembl; ENSG00000182667; Homo sapiens.
CC MIM; 607938; -.
CC GO; GO:0007155; P:cell adhesion; NAS.
CC GO; GO:0008038; P:neuron recognition; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00408; IGC2; 2.
CC PROSITE; PS50835; IG_LIKE; 3.
CC KW Alternative splicing; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;
KW Membrane; Repeat; Signal.
FT SIGNAL 1 33
FT CHAIN 34 321 Neurotrophin.
FT PROPEP 322 344 Removed in mature form (Potential).
FT DOMAIN 39 126 Ig-like C2-type 1.
FT DOMAIN 136 218 Ig-like C2-type 2.
FT DOMAIN 222 309 Ig-like C2-type 3.
FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).
FT CARBOHYD 44 44 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 70 70 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 152 152 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 305 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 305 305 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 321 321 N-linked (GlcNAc...) (Potential).
FT DISULFID 57 115 Potential.
FT DISULFID 157 201 Potential.
FT DISULFID 243 295 Potential.
FT VARSPPLIC 1 27 MGSGGLFPLDKLVVSLRLFLVPT -> MKTIQPKYKH
FT FT SVSWAIFTLGLAALCLFQ (in isoform 2).
FT FT /FTId=VSP 010939.
FT FT PGAV -> ETVL (in isoform 3).
FT VARSPPLIC 313 316

Db 189 QGITREQSGEYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGKGTLCCEASAV 248
Qy 249 PSAEFQWYKDKLEIGKGGKGVKVENPFLSKLFFNNVSEHDYCNVTCVASNKLGHNTNAST 308
Db 249 PSAEFQWYKDKLEIGKGGKGVKVENPFLSKLFFNNVSEHDYCNVTCVASNKLGHNTNAST 308
Qy 309 MLFGPGAVSEVNGTSRRRAGCVMLLLPLLVHLLKLF 344
Db 309 MLFGPGAVSEVNGTSRRRAGCVMLLLPLLVHLLKLF 344

RESULT 5
NTRI RAT STANDARD; PRT; 344 AA.
AC Q627I8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Neurotrophin precursor (GP65).
GN Name=Nt;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 217-229.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=95198094; PubMed=7891157;
RA Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
RA Salzer J.L.;
RT "Cloning of neurotrophin defines a new subfamily of differentially
RT expressed neural cell adhesion molecules.";
RL J. Neurosci. 15:2141-2156(1995).
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Central nervous system.
CC -!- DEVELOPMENTAL STAGE: Expressed at high levels in several
CC developing projection systems; in neurons of the thalamus,
CC subplate, and lower cortical laminae in the forebrain and in the
CC pontine nucleus, cerebellar granule cells, and Purkinje cells in
CC the hindbrain.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U16845; AAA67445.1; -; mRNA.
DR PIR; I56551; I56551
DR Ensembl; ENSRNOG0000023720; Rattus norvegicus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IIG2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT SIGNAL 1 33
FT CHAIN 34 321
FT PROPEP 322 344
FT DOMAIN 39 126
FT DOMAIN 136 218
FT DOMAIN 222 309
FT LIPID 321 321
FT CARBOHYD 44 44
FT N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 70 70
FT CARBOHYD 152 152
FT CARBOHYD 216 216
FT CARBOHYD 284 284
FT CARBOHYD 292 292
FT CARBOHYD 305 305
FT CARBOHYD 321 321
FT DISULFID 57 115
FT DISULFID 157 201
FT DISULFID 243 295
SQ SEQUENCE 344 AA; 37998 MW; CBB39BE53B3B224 CRC64;
Query Match 90.8%; Score 1639.5; DB 1; Length 344;
Best Local Similarity 92.9%; Pred. No. 9.1e-125;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;
Qy 12 ISWALFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCITIDNRVTRVAW 68
Db 9 LPKMKLVVVSLRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCITIDNRVTRVAW 68
Qy 69 LNRSTILYAGNDKWCCLDPRVLLSNLTQYSEIQNVVYVDEGPTCSVQTDNHPKTSRV 128
Db 69 LNRSTILYAGNDKWCCLDPRVLLSNLTQYSEIQNVVYVDEGPTCSVQTDNHPKTSRV 128
Qy 129 HLIQVSPKIVRISDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFVSEDEYLEI 188
Db 129 HLIQVSPKIVRISDISINEGNNISLTCTATGRPEPTVWRHISPKAVGFVSEDEYLEI 188
Qy 189 QGITREQSGDYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGKGTLCCEASAV 248
Db 189 QGITREQSGDYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGKGTLCCEASAV 248
Qy 249 PSAEFQWYKDKLEIGKGGKGVKVENPFLSKLFFNNVSEHDYCNVTCVASNKLGHNTNAST 308
Db 249 PSAEFQWYKDKLEIGKGGKGVKVENPFLSKLFFNNVSEHDYCNVTCVASNKLGHNTNAST 308
Qy 309 MLFGPGAVSEVNGTSRRRAGCVMLLLPLLVHLLKLF 344
Db 309 MLFGPGAVSEVNGTSRRRAGCVMLLLPLLVHLLKLF 344

RESULT 6
Q58DA5 BOVIN
ID Q58DA5 BOVIN PRELIMINARY; PRT; 345 AA.
AC Q58DA5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Neurotrophin.
GN Name=Nt;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Poolled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Partea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RA "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RA libraries and construction of a gene index for cattle.";
RT Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Poolled;
RA Harhay G.P., Sonstegard T.S., Van Tassel C.P., Clawson M.L.,
RA Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
RA "Sequencing and analysis of Bos taurus full-length insert cDNA

```
RT clones.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT021692; AX446539.1; -, mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS0835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 345 AA; 38000 MW; 47C94D781A70F0F7 CRC64;

Query Match          90.6%; Score 1636; DB 2; Length 345;
Best Local Similarity 93.8%; Pred. No. 1.8e-124;
Matches 316; Conservative 5; Mismatches 12; Indels 4; Gaps 2;

QY 12 ISWAIFTGLAALCLF---QGVVRSRGDAPPKAMDNVTVRQGESATLRCCTIDNRVTRVAW 68
DB 9 LPWKCLVVSRLRLFLVPTGVPVRSRGDAPPKAMDNVTVRQGESATLRCCTIDNRVTRVAW 68
QY 69 LNRSTILYAGNDKWCCLDPRVLLSNLTQTSVIEIQNVVYDEGPTCSVQTDNHPKTSRV 128
DB 69 LNRSTILYAGNDKWCCLDPRVLLSNLTQTSVIEIQNVVYDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIVQSPKIVEISSDISINEGNNISLTCTATCRPEPTVTRHISPKAVGFVSEDEYLEI 188
DB 129 HLIVQSPKIVEISSDISINEGNNISLTCTATCRPEPTVTRHISPKAVGFVSEDEYLEI 188
QY 189 QGITRQSGDYECASNDVAAPVRRVKVTNYPPIYISAKGTGVPVGKGLTLCQASAV 248
DB 189 QGITRQSGDYECASNDVAAPVRRVKVTNYPPIYISAKGTGVPVGKGLTLCQASAV 248
QY 249 PSAEFQYKDDKRLIEGKGVKVENRPFLLKLIFFNVSEHDYNYTCVASNKLGHNTNASI 308
DB 249 PSAEFQYKDDKRLIEGKGVKVENRPFLLKLIFFNVSEHDYNYTCVASNKLGHNTNASI 308
QY 309 MLFGPGAVSEVNGT--SRRAGCVWLLPLLVHLHLKPF 344
DB 309 TLFGPGAVSEVNGTSSRRAGCLWLLPLLVHLHLKPF 345

RESULT 7
CEPU1_CHICK
ID CEPU1_CHICK STANDARD; PRT; 353 AA.
AC Q90773;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CEPU-1 protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC MEDLINE=96370549; PubMed=8774445;
RX Spalman F., Bruemendorf T.;
RT "CEPU-1, a novel immunoglobulin superfamily molecule, is expressed by
RT developing cerebellar Purkinje cells."
RL J. Neurosci. 16:1770-1779(1996).
CC -!- FUNCTION: It may be a cellular address molecule specific to
CC Purkinje cells. It may represent a receptor or a subunit of a
CC receptor complex.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Minor;
CC IsoId=Q90773-1; Sequence=Displayed;
CC Name=2; Synonyms=Major;
CC IsoId=Q90773-2; Sequence=VSP_002607;

CC -!- TISSUE SPECIFICITY: Found on the dendrites, somata and axons of
CC developing Purkinje cells. Undetectable on other neurons like
CC Golgi or granule cells.
CC -!- DEVELOPMENTAL STAGE: Expressed by developing cerebellar Purkinje
CC cells. Expression coincides with the growth of the dendritic tree,
CC after Purkinje cells have finished their migration from the
CC ventricular zone (from E15 until E21). Expressed in the adult.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; Z72497; CA96578.1; -, mRNA.
DR Ensembl; ENSGALG0000001437; Gallus gallus.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS0835; IG_LIKE; 3.
KW Alternative splicing; Cell adhesion; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT SIGNAL 1 28
FT CHAIN 29 330
FT PROPEP 331 353
FT DOMAIN 37 124
FT DOMAIN 134 216
FT DOMAIN 220 314
FT LIPID 330 330
FT CARBOHYD 42 42
FT CARBOHYD 68 68
FT CARBOHYD 150 150
FT CARBOHYD 282 282
FT CARBOHYD 290 290
FT CARBOHYD 303 303
FT DISULFID 55 113
FT DISULFID 155 199
FT DISULFID 241 293
FT VARSPLIC 310 320
FT SEQUENCE 353 AA; 38736 MW; 2550C48591EBBBA6 CRC64;
Query Match          81.8%; Score 1477.5; DB 1; Length 353;
Best Local Similarity 78.6%; Pred. No. 1.4e-111;
Matches 276; Conservative 32; Mismatches 32; Indels 11; Gaps 1;

QY 5 QPKMNSISWAIFTGLAALCLFQGVVRSRGDAPPKAMDNVTVRQGESATLRCCTIDNRVT 64
DB 3 QAKMQHPVSVWIFAGWAALLLFQGVVRSRGDAPPKAMDNVTVRQGESATLRCSDNRVT 62
QY 65 RVAVLNRSTILYAGNDKWCCLDPRVLLSNLTQTSVIEIQNVVYDEGPTCSVQTDNHPK 124
DB 63 RVAVLNRSTILYAGNDKWCCLDPRVLLSNLTQTSVIEIQNVVYDEGPTCSVQTDNHPK 122
QY 125 TSVRHILVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDE 184
DB 123 TSVRHILVQVSPKIVEISSDISINEGNNISLTCTATGRPDPTITWRHISPKAVGFISEDE 182
QY 185 YLEIQTITREQSGDYECASNDVAAPVRRVKVTNYPPIYISAKGTGVPVGKGLTQCE 244
DB 183 YLEITGITREQSGDYECASNDVAAPVRRVKVTNYPPIYISAKSTGVPVGKGLMCE 242
QY 245 ASAVPSAEFQYKDDKRLIEGKGVKVENRPFLLKLIFFNVSEHDYNYTCVASNKLGH 304
DB 243 ASAVPSAEFQYKDDKRLIEGKGVKVENRPFLLKLIFFNVSEHDYNYTCVASNKLGH 302
QY 305 NASIMLF-----GPGAVSVSNGTSRRAGCVWLLPLLVHLHLKPF 344
```

Db 303 NASMILYBETTTALTTPWKGFVHDGNSGAWRRGSCAWLLALPLAQLARQF 353

```

RESULT 8
O57596_CHICK PRELIMINARY; PRT; 313 AA.
AC O57596;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Neural secreted glycoprotein (CEPU-Se alpha 2 isoform).
GN Names:CEPU; Synonyms:CEPU-Se;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99347334; PubMed=10420985;
RA Kim D.S., Rhew T.H., Moss D.J., Kim J.Y.;
RT "cDNA cloning of the CEPUSe, a secreted type of neural glycoprotein
RT belonging to the immunoglobulin-like opioid binding cell adhesion
RT molecule (OSCAM) subfamily.";
RL Mol. Cells 9:270-276(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kim D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225897; CAA12649.1; -; Genomic_DNA.
DR EMBL; AF292935; AAG01878.1; -; mRNA.
DR HSSP; Q9UQH9; 1DJS.
DR Ensembl; ENSGALG0000001437; Gallus gallus.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 313 AA; 34482 MW; 99AD825CAB4A5347 CRC64;

Query Match 79.1%; Score 1428; DB 2; Length 313;
Best Local Similarity 85.4%; Pred. No. 1.3e-107;
Matches 263; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 5 OPHKNSISWAIITGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVT 64
DB 3 QAKQHVPVSVIFAGMAALLFQGVPRSGDATFPKAMDNVTVRQGESATLRCSVDNRVT 62
QY 65 RVAWLNRSTLYAGNDKWCCLDRVLLSNTQTOYSTIIONVDVYDEGPTCSVQTDNHPK 124
DB 63 RVAWLNRSTLYAGNDKWCCLDRVLLSNTQTOYSTIIONVDVYDEGPTCSVQTDNHPK 122
QY 125 TSVRLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDE 184
DB 123 TSVRLIVQSPKITEISSDISINEGNNISLTCTATGRPDPTITWRHISPKAVGFISEDE 182
QY 185 YLEIQITRQSGDYECASNDVAAPVVRVKVTNNYPPYISAKGTGVPVGKGLQCE 244
DB 183 YLEITGITRQSGDYECASNDVAAPVVRVKVTNNYPPYISAKSTGVPVGKGLMCE 242
QY 245 ASAVPSAEFWYKDDKRLIEGKGVKVENRPFSLIFFNVSHEHDYGNVTCVASNKLIGHT 304
DB 243 ASAVPSADFQWKDDKRLAEGQGLKVENKAFPSRLTFFNVSEQDYGNTTCVASNQLGNT 302
QY 305 NASIMLFG 312
DB 303 NASMILYG 310

```

```

RESULT 9
O93242_CHICK PRELIMINARY; PRT; 344 AA.
AC O93242;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE CEPU-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011810; BAA31514.1; -; mRNA.
DR HSSP; Q9UQH9; 1DJS.
DR Ensembl; ENSGALG0000001437; Gallus gallus.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 344 AA; 37614 MW; 22CAA8F526A6B57E CRC64;

Query Match 79.0%; Score 1427.5; DB 2; Length 344;
Best Local Similarity 79.2%; Pred. No. 1.6e-107;
Matches 267; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 11 STSWAIFTGLAALCLP---QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRA 67
DB 8 ALPWRCLVVLCLRLFLVPAGVPRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRA 67
QY 68 WLNRSITLYAGNDKWCCLDRVLLSNTQTOYSTIIONVDVYDEGPTCSVQTDNHPKTSR 127
DB 68 WLNRSITLYAGNDKWCCLDRVLLSNTQTOYSTIIONVDVYDEGPTCSVQTDNHPKTSR 127
QY 128 VHLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLE 187
DB 128 VHLIVQSPKITEISSDISINEGNNISLTCTATGRPDPTITWRHISPKAVGFISEDEYLE 187
QY 188 IQGITRQSGDYECASNDVAAPVVRVKVTNNYPPYISAKGTGVPVGKGLQCEASA 247
DB 188 ITGITRQSGDYECASNDVAAPVVRVKVTNNYPPYISDAKSTGVPVGKGLMCEASA 247
QY 248 VPSAEFWYKDDKRLIEGKGVKVENRPFSLIFFNVSHEHDYGNVTCVASNKLIGHTNAS 307
DB 248 VPSADFQWKDDKRLAEGQGLKVENKAFPSRLTFFNVSEQDYGNTTCVASNQLGNTNAS 307
QY 308 IMLPFGFVSEVSNSTSRAGCVWLLPLVLLHLLKF 344
DB 308 MILYGFVHDGNSGAWRRGSCAWLLALPLAQLARQF 344

RESULT 10
O9DG15_CHICK PRELIMINARY; PRT; 315 AA.
AC O9DG15;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE CEPU-Se alpha 1 isoform.
GN Name:CEPU-Se;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

```



```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF292936; AAG01879.1; -; mRNA.
DR HSP; G9UQH9; 1DJS.
DR Ensembl; ENSGALG0000001437; Gallus gallus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 315 AA; 34606 MW; 68C5D27F0DDC6FB2 CRC64;

Query Match 75.2%; Score 1357.5; DB 2; Length 315;
Best Local Similarity 83.0%; Pred. No. 6.8e-102;
Matches 253; Conservative 26; Mismatches 23; Indels 3; Gaps 1;

QY 11 SLSWAIFTGLAALCLF---GGVPVRSGDATFPKAMNDVTVRQGESATLRCCTIDNRVTRVA 67
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
8 ALPWRCLVLLCLRLFLVPAGVPVRSGDATFPKAMNDVTVRQGESATLRCSDNRVTRVA 67
QY 68 WLNRSILYAGNDKCLDRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSR 127
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
68 WLNRSILYAGNDKCLDRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSR 127
QY 128 VHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLE 187
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
128 VHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLE 187
QY 188 IGITREQSGDYECASNDVAAPVVRVKVTNYPPIYSEAKGTGVPVQKGTLOCEASA 247
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
188 IGITREQSGDYECASNDVAAPVVRVKVTNYPPIYSEAKGTGVPVQKGTLOCEASA 247
QY 248 VPSAEQWYKDKRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 307
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
248 VPSAEQWYKDKRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 307
QY 308 IMLFG 312
Db ::::
308 MLYG 312

RESULT 11
Q6DFY2 MOUSE
ID Q6DFY2_MOUSE PRELIMINARY; PRT; 337 AA.
AC Q6DFY2_
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Opioid binding protein/cell adhesion molecule-like.
GN Name=Opcml;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
```

```

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076581; AAH76581.1; -; mRNA.
DR MGI; MGI:97397; Opcml.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 337 AA; 37156 MW; 2A279D982E60F4B CRC64;

Query Match 72.3%; Score 1306; DB 2; Length 337;
Best Local Similarity 72.1%; Pred. No. 1.1e-97;
Matches 243; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

QY 8 MHSISWAIFTGLAALCLFQGVVRSGDATFPKAMNDVTVRQGESATLRCCTIDNRVTRVA 67
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1 MYHPAYTWVFSATTALLFIPGVVRSGDATFPKAMNDVTVRQGESATLRCCTIDNRVTRVA 60
QY 68 WLNRSILYAGNDKCLDRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSR 127
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
61 WLNRSILYAGNDKCLDRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSR 120
QY 128 VHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGVSEDEYLE 187
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
121 VHLIVQSPKIVEISSDISITVNEGSVTLCLAIAGRPEPTVTRHLSVKGQGVSEDEYLE 180
QY 188 IGITREQSGDYECASNDVAAPVVRVKVTNYPPIYSEAKGTGVPVQKGTLOCEASA 247
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
181 ISDIKRDQSGEYECASNDVAAPVVRVKVTNYPPIYSEAKGTGVPVQKGTLOCEASA 240
QY 248 VPSAEQWYKDKRLTEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTAS 307
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
241 VPMAEFQWFKEDTRLATGLDGVRIENKGRISTLTFFNVSEKDYGNVTCVATNKLGNNTAS 300
QY 308 IMLFGAVSEVNSGTSTRAGCVLLPLLVLLHLKLF 344
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
301 ITLYGFGAVIDGWSASRALACLWLSGTFFAHFFIKF 337

RESULT 12
OBSCAM CHICK
ID OBSCAM_CHICK STANDARD; PRT; 337 AA.
AC Q98892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Opioid binding protein/cell adhesion molecule homology precursor
DE (Neurite inhibitor GP55-A) (OBSCAM protein gamma isoform).
GN Name=OPCML;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```


RC TISSUE=Brain;
RA Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
RT "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM CDNAS from
RT chick: structural diversity of IGLON family proteins.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 64-337, AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97157768; PubMed=9004047;
RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT are members of the Ig superfamily and are related to OBCAM,
RT neurotrophin, LAMP and CEPU-1";
RL J. Cell Sci. 109:3129-3138(1996).
CC -1- FUNCTION: Inhibits neurite outgrowth.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -1- DEVELOPMENTAL STAGE: Increases during development from very low
CC levels at embryonic day 10 and is most abundant after hatching.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -1- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Y08170; CAB41420.1; -; mRNA.
DR HSP; P78310; IP5W.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 314
FT FT
FT PROPEP 315 337
FT DOMAIN 32 119
FT DOMAIN 129 211
FT DOMAIN 215 302
FT LIPID 314 314
FT FT
FT CARBOHYD 133 133
FT CARBOHYD 277 277
FT CARBOHYD 285 285
FT CARBOHYD 298 298
FT DISULFID 50 108
FT DISULFID 150 194
FT DISULFID 236 288
SQ SEQUENCE 337 AA; 36887 MW; BAE717551856651E CRC64;

Query Match 72.3%; Score 1305; DB 1; Length 337;
Best Local Similarity 73.2%; Pred. No. 1.4e-97;
Matches 248; Conservative 34; Mismatches 53; Indels 4; Gaps 2;

QY 8 MHSISWAIPTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVA 67
DB 1 MYHPACWIVTATALLFIPGVPRSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVA 60

QY 68 WLNRSITLYAGNDKWCIDPRVLLSNTQYISIEIONVDVYDEGPTCSVQTDNHPKTSR 127
DB 61 WLNRSITLYAGNDKWSIDNRVLLSNTQYISIKIHNVVDVYDEGPTCSVQTDNHPKTSR 120

QY 128 VHLIVVSPKIVEISSISINEGNISLTCTIATCRPEPTVTRHISPK-AVGFSVEDEYL 187
DB 121 VHLIVVPPQIVNISSDITVNEGSSVTLMLCIAFGRPEPTVTRHLSGKGQGVSEDEYLE 180

QY 188 IQGITREQSGDYECASNDVAAPVVRVKVTVNPPYISEAKGTGVPVQKGTLCQCEASA 247

DB 181 ITGITREQSGDYECASNDVAAPVVRVKVTVNPPYISNAKNKTGASVQKGLQCEASA 240
QY 248 VPSAEFQWKDKRLLEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTAS 307
DB 241 VPAVEFQWFKEDTRLANGLEGVRIESKGRSLTILTFENVSEKDYGNVTCVATNKLGNNTAS 300
QY 308 IMLFGGAVSEVSNGTSTRAG--CVWLLPLLVLLHLLKF 344
DB 301 IILYGGGAVHSDGNAASRAAGGLCW--ATLLARLLLDLF 337

RESULT 13
Q723W6_HUMAN
ID Q723W6_HUMAN PRELIMINARY; PRT; 338 AA.
AC Q723W6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp668H1949.
GN Name=DKFZp668H1949;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human amygdala;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
DR EMBL; BX537377; CAD97619.1; -; mRNA.
DR HSP; Q9U0H9; 111L.
DR Ensemble; ENSG00000183715; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 338 AA; 37267 MW; EDD86EEZC57B09E3 CRC64;

Query Match 71.7%; Score 1295.5; DB 2; Length 338;
Best Local Similarity 71.6%; Pred. No. 8.2e-97;
Matches 242; Conservative 38; Mismatches 57; Indels 1; Gaps 1;

QY 8 MHSISWAIPTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVA 67
DB 1 MYHPAYWVFSATTALLFIPGVPRSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVA 60

QY 68 WLNRSITLYAGNDKWCIDPRVLLSNTQYISIEIONVDVYDEGPTCSVQTDNHPKTSR 127
DB 61 WLNRSITLYAGNDKWSIDPRVLLSNTQYISIQNVVDVYDEGPTCSVQTDNHPKTSR 120

QY 128 VHLIVVSPKIVEISSISINEGNISLTCTIATCRPEPTVTRHISPK-AVGFSVEDEYL 186
DB 121 VHLIVVPPQIVNISSDITVNEGSSVTLMLCIAFGRPEPTVTRHLSVKEGGFVSEDEYL 180

QY 187 IQGITREQSGDYECASNDVAAPVVRVKVTVNPPYISEAKGTGVPVQKGTLCQCEAS 246
DB 181 EISDIKRDQSGDYECASNDVAAPVVRVKVTVNPPYISAKAKNTGVSQKGLSCEAS 240

QY 247 AVPSAEFQWKDKRLLEGKKGKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTA 306
DB 241 AVPMAEFQWFKEDTRLATGLDGRNENKGRMSTLTTFENVSEKDYGNVTCVATNKLGNNTA 300

QY 307 SIMLFGGAVSEVSNGTSTRAGCVWLLPLLVLLHLLKF 344
DB 301 SITLYGGGAVIDGWSASRALALWLSGTLAAHFFIKF 338

RESULT 14

```
Q5R7T4 PONPY
ID Q5R7T4_PONPY PRELIMINARY; PRT; 338 AA.
AC Q5R7T4.
DT 01-FEB-2005 (T-EMBLrel. 29, Created)
DT 01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFp459M0925.
GN Name=DKFp459M0925;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]_TaxID=9600;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR860025; CA92176.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG. 1.
DR SMART; SM00409; IG. 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 338 AA; 37267 MW; EDD86EE2C57B09E3 CRC64;

Query Match 71.7%; Score 1295.5; DB 2; Length 338;
Best Local Similarity 71.6%; Pred. No. 8.2e-97;
Matches 242; Conservative 38; Mismatches 57; Indels 1; Gaps 1;

QY 8 MHNSISWAIPTGLAALCLFGVVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRA 67
DB 1 MYHPAIVVPSATTALLFIPGVVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRA 60
QY 68 WLNRSITLYAGNDKWCIDPRVLLSNTQYTSIEIQNVVDYDGGPYTCVQTDNHPKTSR 127
DB 61 WLNRSITLYAGNDKWCIDPRVILVNTPTQYSIMIQNVVDYDGGPYTCVQTDNHPKTSR 120
QY 128 VHLIVQVSPKIVISSDISINEGNISLTCIATGRPEPTVWRHISPK-avgfvsdeyl 186
DB 121 VHLIVQVPPQIMNISSDITVNEGSSVLLCLALGRPEPTVWRHLSVKGQGGVSEYIL 180
QY 187 EIQGITREOSGDYECASNDVAAPVVRVVKVTVNPPYIIEAKGTGVPVQKGTLOCEAS 246
DB 181 EISDIKRDQSGEYECASALNDVAAPVVRVVKVTVNPPYIIEAKGTGVPVQKGTLOCEAS 240
QY 247 AVPSAEFQYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTA 306
DB 241 AVPMABFQWKEETRLATGLDGMRIENKGRMSTLTFFNVSEKDYGYNTCVATNKLGNNTA 300
QY 307 SIMLFGPGAVSEVSNCTSRACGVLLPLVHLHLKPF 344
DB 301 SITLYGPGAVIDGVNSASRALACLWLSTGLLAHFFIKF 338

RESULT 15
Q6GM08 XENLA
ID Q6GM08_XENLA PRELIMINARY; PRT; 345 AA.
AC Q6GM08;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE MGC84065 protein.
GN Name=MGC84065;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
```

```
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC074283; AAH74283.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG. 2.
DR SMART; SM00409; IG. 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 345 AA; 38167 MW; C2BEE4F5A2EECA6 CRC64;

Query Match 70.7%; Score 1276.5; DB 2; Length 345;
Best Local Similarity 71.7%; Pred. No. 3e-95;
Matches 243; Conservative 43; Mismatches 44; Indels 9; Gaps 2;

QY 12 ISWAIPTGLAALCLF-----QGVVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTR 65
DB 1 MGFAPWRLLALCLLFLVPAGVVRSGDAGFPKAMDNVTVRQGD SATLRCTIDNRVTR 60
QY 66 VAWLNRSITLYAGNDKWCIDPRVLLSNTQYTSIEIQNVVDYDGGPYTCVQTDNHPKPT 125
DB 61 VAWLNRSITLYAGNDKWCIDPRVLLANTKSQYSIEIQNVDIYDGGPYTCVQTDNHPKPT 120
QY 126 SRVHLIVQVSPKIVISSDISINEGNISLTCIATGRPEPTVWRHISPKAVGFVSEDEY 185
DB 121 SRVHLIVQVPPRIVDISNIAVNEGSVSLICATGRPEPVVWRVYLSPKARGFVSEDSY 180
QY 186 LEIQGITREOSGDYECASNDVAAPVVRVVKVTVNPPYIIEAKGTGVPVQKGTLOCEA 245
DB 181 LEITGITREOSGIYECASNDVSPDVRVRKLVTVNPPYIIPVYLLDAQINQIAPLHGRHILQCEA 240
QY 246 SAVPSAEFQYKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTN 305
```

Db 241 SAVPAADFFWYKEDKRLSDSWRGVKVENRETYSRVTFNLNVSEQDYGNVTCMAKNLLGHSN 300
Qy 306 ASIMLFPGGAVSEVSNVSGTSSRRAGCVWLLPLLVHLLKPF 344
Db 301 ASIILFPGGAVHDGNSGSPQ---CPFCAPLLLLLLLLLPF 336

Search completed: February 7, 2006, 16:47:43
Job time : 278 secs

This Page Blank (uspto)